

Connecting via Winsock to STN

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LOGINID:SSSPTA1642GXN

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	Jun 03	New e-mail delivery for search results now available
NEWS	4	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS	5	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS	6	Aug 26	Sequence searching in REGISTRY enhanced
NEWS	7	Sep 03	JAPIO has been reloaded and enhanced
NEWS	8	Sep 16	Experimental properties added to the REGISTRY file
NEWS	9	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS	10	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS	11	Oct 24	BEILSTEIN adds new search fields
NEWS	12	Oct 24	Nutraceuticals International (NUTRACEUT) now available on STN
NEWS	13	Nov 18	DKILIT has been renamed APOLLIT
NEWS	14	Nov 25	More calculated properties added to REGISTRY
NEWS	15	Dec 04	CSA files on STN
NEWS	16	Dec 17	PCTFULL now covers WP/PCT Applications from 1978 to date
NEWS	17	Dec 17	TOXCENTER enhanced with additional content
NEWS	18	Dec 17	Adis Clinical Trials Insight now available on STN
NEWS	19	Jan 29	Simultaneous left and right truncation added to COMPENDEX, ENERGY, INSPEC
NEWS	20	Feb 13	CANCERLIT is no longer being updated
NEWS	21	Feb 24	METADEX enhancements
NEWS	22	Feb 24	PCTGEN now available on STN
NEWS	23	Feb 24	TEMA now available on STN
NEWS	24	Feb 26	NTIS now allows simultaneous left and right truncation
NEWS	25	Feb 26	PCTFULL now contains images
NEWS	26	Mar 04	SDI PACKAGE for monthly delivery of multifile SDI results
NEWS	27	Mar 20	EVENTLINE will be removed from STN
NEWS	28	Mar 24	PATDPAFULL now available on STN
NEWS	29	Mar 24	Additional information for trade-named substances without structures available in REGISTRY
NEWS	30	Apr 11	Display formats in DGENE enhanced
NEWS	31	Apr 14	MEDLINE Reload
NEWS	32	Apr 17	Polymer searching in REGISTRY enhanced
NEWS	33	Jun 13	Indexing from 1947 to 1956 added to records in CA/CAPLUS
NEWS	34	Apr 21	New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX
NEWS	35	Apr 28	RDISCLOSURE now available on STN
NEWS	36	May 05	Pharmacokinetic information and systematic chemical names added to PHAR
NEWS	37	May 15	MEDLINE file segment of TOXCENTER reloaded
NEWS	38	May 15	Supporter information for ENCOMPPAT and ENCOMPLIT updated
NEWS	39	May 16	CHEMREACT will be removed from STN
NEWS	40	May 19	Simultaneous left and right truncation added to WSCA
NEWS	41	May 19	RAPRA enhanced with new search field, simultaneous left and right truncation
NEWS	42	Jun 06	Simultaneous left and right truncation added to CBNB

NEWS 43 Jun 06 PASCAL enhanced with additional data
NEWS 44 Jun 20 2003 edition of the FSTA Thesaurus is now available
NEWS 45 Jun 25 HSDB has been reloaded

NEWS EXPRESS April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT
MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
AND CURRENT DISCOVER FILE IS DATED 01 APRIL 2003
NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
NEWS PHONE Direct Dial and Telecommunication Network Access to STN
NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

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of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 15:05:12 ON 27 JUN 2003

=> file .gary

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 15:05:17 ON 27 JUN 2003

FILE 'CANCERLIT' ENTERED AT 15:05:17 ON 27 JUN 2003

FILE 'BIOSIS' ENTERED AT 15:05:17 ON 27 JUN 2003

COPYRIGHT (C) 2003 BIOLOGICAL ABSTRACTS INC.(R)

FILE 'EMBASE' ENTERED AT 15:05:17 ON 27 JUN 2003

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FILE 'SCISEARCH' ENTERED AT 15:05:17 ON 27 JUN 2003

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=> 59D8

59D8 IS NOT A RECOGNIZED COMMAND

The previous command.name entered was not recognized by the system.

For a list of commands available to you in the current file, enter

"HELP COMMANDS" at an arrow prompt (=>).

=> s 59D8

L1 117 59D8

=> s l1 and monoclonal

L2 89 L1 AND MONOCLONAL

=> s l2 and py<=1997

2 FILES SEARCHED...

4 FILES SEARCHED...

L3 83 L2 AND PY<=1997

=> s l3 and (cancer? or ?carcinoma or neoplas? or tumour? or tumor? or metast?)

2 FILES SEARCHED...

L4 2 L3 AND (CANCER? OR ?CARCINOMA OR NEOPLAS? OR TUMOUR? OR TUMOR?)

OR METAST?)

=> dup rem l4

PROCESSING COMPLETED FOR L4

L5 1 DUP REM L4 (1 DUPLICATE REMOVED)

=> d ibib abs

L5 ANSWER 1 OF 1 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 93190305 MEDLINE
DOCUMENT NUMBER: 93190305 PubMed ID: 8446952
TITLE: High-level expression of antibody-plasminogen activator
fusion proteins in hybridoma cells.
AUTHOR: Love T W; Quertermous T; Zavodny P J; Runge M S; Chou C C;
Mullins D; Huang P L; Schnee J M; Kestin A S; Savard C E; +
CORPORATE SOURCE: Massachusetts General Hospital, Boston 02114.
CONTRACT NUMBER: HL-02414 (NHLBI)
HL-19259 (NHLBI)
SOURCE: THROMBOSIS RESEARCH, (1993 Jan 15) 69 (2) 221-9.
Journal code: 0326377. ISSN: 0049-3848.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199304
ENTRY DATE: Entered STN: 19930416
Last Updated on STN: 19930416
Entered Medline: 19930408

AB We show that the mouse gamma 2b heavy chain or human beta-globin 3'
untranslated region can greatly enhance protein expression in myeloma
cells transfected by genes coding for antibody-plasminogen activator
fusion proteins. Expression plasmids were constructed containing a cloned
genomic heavy chain variable region from fibrin-specific
monoclonal antibody **59D8**, a cloned genomic constant
region of the mouse gamma 2b heavy chain, and DNA sequence coding for
either tissue-type plasminogen activator (tPA) or a segment of urokinase
(UK) and their respective 3' untranslated sequences. Cell lines
transfected with these constructs, pSVtPA (tPA) and pSVUKG(UK), produced
extremely low levels of mRNA and protein (0.008-0.06 micrograms/ml) in
comparison with the parental **59D8** myeloma cell line (7.6-10
micrograms/ml). In vitro nuclear run-off analysis indicated that the low
steady-state levels of mRNA encoded by pSVUKG(UK) did not result from a
lower rate of transcription of the transfected gene (relative to the rate
of transcription of the endogenous heavy chain gene in the **59D8**
parent cells). In an attempt to increase protein secretion, we assembled
the expression plasmids pSVtPA(Ig), pSVUKG(Ig), and pSVUKG(beta), in which
the 3' untranslated region of the mouse gamma 2b heavy chain or human
beta-globin gene was substituted for the 3' untranslated region of the
plasminogen activator gene. Analysis of supernatant media from cell lines
transfected with these constructs showed an increase in recombinant
protein secretion of 68 to 100 fold in comparison with that from cell
lines transfected with pSVtPA(tPA) or pSVUKG(UK).

=> d his

(FILE 'HOME' ENTERED AT 15:05:12 ON 27 JUN 2003)

FILE 'MEDLINE, CANCERLIT, BIOSIS, EMBASE, SCISEARCH' ENTERED AT 15:05:17
ON 27 JUN 2003

L1 117 S 59D8
L2 89 S L1 AND MONOCLONAL
L3 83 S L2 AND PY<=1997
L4 2 S L3 AND (CANCER? OR ?CARCINOMA OR NEOPLAS? OR TUMOUR? OR TUMO

L5

1 DUP REM L4 (1 DUPLICATE REMOVED)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:02:14 ; Search time 10.2667 Seconds
(without alignments)
20.061 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41

Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	7	1	US-08-058-699-10
2	41	100.0	8	1	US-08-058-699-11
3	41	100.0	10	2	US-08-448-547-1
4	41	100.0	28	1	US-08-486-135-12
5	41	100.0	28	1	US-08-470-152-12
6	41	100.0	28	2	US-08-468-964B-10
7	41	100.0	28	2	US-07-871-282A-10
8	41	100.0	28	2	US-08-290-853-33
9	41	100.0	28	2	US-08-253-678A-10
10	41	100.0	28	3	US-08-582-134B-10
11	41	100.0	28	3	US-08-170-299-10
12	41	100.0	30	2	US-08-290-853-35
13	41	100.0	31	1	US-08-472-535-9
14	41	100.0	31	1	US-08-484-774-9
15	41	100.0	31	3	US-08-266-178A-9
16	41	100.0	491	1	US-08-206-176-4
17	31	75.6	66	4	US-09-177-249-296
18	31	75.6	170	1	US-08-227-372-1
19	31	75.6	170	6	5194425-3
20	31	75.6	215	1	US-08-107-684B-9
21	31	75.6	215	1	US-08-107-684B-13
22	31	75.6	219	4	US-09-134-001C-4644
23	30	73.2	21	1	US-08-507-124-4
24	30	73.2	117	4	US-09-199-637A-33
25	30	73.2	253	4	US-09-180-109A-35
26	30	73.2	254	4	US-09-180-109A-31
27	30	73.2	358	2	US-08-558-823-19

28	30	73.2	453	4	US-09-163-444-2	Sequence 2, Appli
29	30	73.2	899	1	US-08-365-689-2	Sequence 2, Appli
30	30	73.2	899	1	US-08-145-138A-2	Sequence 2, Appli
31	30	73.2	911	1	US-08-596-985-2	Sequence 2, Appli
32	30	73.2	933	1	US-07-747-781-2	Sequence 2, Appli
33	30	73.2	933	5	PCT-US92-06888-2	Sequence 2, Appli
34	30	73.2	2547	3	US-09-058-489-35	Sequence 35, Appli
35	30	73.2	2555	3	US-09-058-489-36	Sequence 36, Appli
36	29	70.7	63	4	US-09-072-596-284	Sequence 284, App
37	29	70.7	200	4	US-09-298-731-32	Sequence 32, Appl
38	29	70.7	256	4	US-09-399-913-32	Sequence 32, Appl
39	29	70.7	343	3	US-08-978-741-17	Sequence 17, Appl
40	29	70.7	343	4	US-09-333-729A-13	Sequence 13, Appl
41	29	70.7	365	3	US-08-978-741-2	Sequence 2, Appli
42	29	70.7	365	4	US-09-333-729A-3	Sequence 3, Appli
43	29	70.7	397	3	US-08-978-741-6	Sequence 6, Appli
44	29	70.7	397	4	US-09-333-729A-7	Sequence 7, Appli
45	29	70.7	432	4	US-09-443-041A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-058-699-10
; Sequence 10, Application US/08058699
; Patent No. 5443827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marschall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-058-699-10

Query Match 100.0%; Score 41; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 2

US-08-058-699-11
; Sequence 11, Application US/08058699
; Patent No. 5443627
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marschall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-058-699-11

Query Match 100.0%; Score 41; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 3

US-08-448-547-1
; Sequence 1, Application US/08448547
; Patent No. 5821068
; GENERAL INFORMATION:
; APPLICANT: Soe, Gilbu
; APPLICANT: Kohno, Isao
; APPLICANT: Inuzuka, Kimiko
; APPLICANT: Ito, Yumiko
; TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
; TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,547
FILING DATE: 30-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01844
FILING DATE: 01-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-297325
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-38931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-547-1

Query Match 100.0%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 4

US-08-486-135-12
; Sequence 12, Application US/08486135
; Patent No. 5720934
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/486,135

;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5720934nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,205-N
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-486-135-12

Query Match 100.0%; Score 41; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 5
US-08-470-152-12
;; Sequence 12, Application US/08470152
;; Patent No. 5780007
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T
;; APPLICANT: Buttram, Scott
;; APPLICANT: McBride, William
;; APPLICANT: Lister-James, John
;; APPLICANT: Civitello, Edgar R
;; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
;; TITLE OF INVENTION: Imaging
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive, Suite 3000
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/470,152
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5780007nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,205-L
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1234
;; TELEFAX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-470-152-12

Query Match 100.0%; Score 41; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 6
US-08-468-964B-10
;; Sequence 10, Application US/08468964B
;; Patent No. 5923303
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T.
;; APPLICANT: Buttram, Scott
;; APPLICANT: McBride, William
;; APPLICANT: Lister-James, John
;; APPLICANT: Civitello, Edgar R.
;; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
;; TITLE OF INVENTION: Imaging
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Diatide, Inc.
;; STREET: 9 Delta Drive
;; CITY: Londonderry
;; STATE: NH
;; COUNTRY: USA
;; ZIP: 03053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,964B
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDaniel, Patricia A.
;; REGISTRATION NUMBER: 33,194
;; REFERENCE/DOCKET NUMBER: DITI 111D4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (603) 437-8970
;; TELEFAX: (603) 437-8977
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-468-964B-10

Query Match 100.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 1 GHRPLDK 7

RESULT 7
US-07-871-282A-10
;; Sequence 10, Application US/07871282A
;; Patent No. 5965107
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T.
;; APPLICANT: Buttram, Scott
;; APPLICANT: McBride, William
;; APPLICANT: Lister-James, John
;; APPLICANT: Civitello, Edgar R.
;; TITLE OF INVENTION: Technetium-99m Labeled Peptides for

;; TITLE OF INVENTION: Imaging
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Diatide, Inc.
;; STREET: 9 Delta Drive
;; CITY: Londonderry
;; STATE: NH
;; COUNTRY: USA
;; ZIP: 03053
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/871.282A
;; FILING DATE: 20-APR-1992
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDaniel, Patricia A.
;; REGISTRATION NUMBER: 33,194
;; REFERENCE/DOCKET NUMBER: DITI 111
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (603) 437-8970
;; TELEFAX: (603) 437-8977
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
US-07-871-282A-10

Query Match 100.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 8
US-08-290-853-33
;; Sequence 33, Application US/08290853
;; Patent No. 5989519
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T
;; APPLICANT: Buttram, Scott
;; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
;; TITLE OF INVENTION: Imaging Inflammation
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive, Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/290,853
;; FILING DATE: 11-OCT-1994
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No 5989519nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,112-H

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /label= BAT
;; OTHER INFORMATION: /note= "The amino terminus is linked to a BAT
;; OTHER INFORMATION: radiolabel binding moiety."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 28
;; OTHER INFORMATION: /label= Amide
;; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
;; OTHER INFORMATION: amide"
;;
US-08-290-853-33

Query Match 100.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 9
US-08-253-678A-10
;; Sequence 10, Application US/08253678A
;; Patent No. 5997844
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T.
;; APPLICANT: Buttram, Scott.
;; APPLICANT: McBride, William
;; APPLICANT: Lister-James, John
;; APPLICANT: Civitello, Edgar R.
;; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
;; TITLE OF INVENTION: IMAGING
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Diatide, Inc.
;; STREET: 9 Delta Drive
;; CITY: Londonderry
;; STATE: NH
;; COUNTRY: USA
;; ZIP: 03053
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/253,678A
;; FILING DATE: 03-JUN-1994
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDaniel, Patricia A.
;; REGISTRATION NUMBER: 33,194
;; REFERENCE/DOCKET NUMBER: DITI 112
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (603) 437-8970
;; TELEFAX: (603) 437-8977
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid

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; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-253-678A-10
Query Match 100.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 10
US-08-582-134B-10
; Sequence 10, Application US/08582134B
; Patent No. 6074627
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 112D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-582-134B-10
Query Match 100.0%; Score 41; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 11
US-08-170-299-10
; Sequence 10, Application US/08170299
; Patent No. 6086849
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,299
; FILING DATE: 09-FEB-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6086849nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-170-299-10
Query Match 100.0%; Score 41; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 12
US-08-290-853-35
; Sequence 35, Application US/08290853
; Patent No. 5989519
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,853
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; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5989519nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Picollinoyl
; OTHER INFORMATION: /note= "The amino terminal residue is
; OTHER INFORMATION: pyridine-2-carboxyl; the thiol of the cysteine is
; OTHER INFORMATION: protected by an acetamidomethyl group."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 30
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; OTHER INFORMATION: amide"
; US-08-290-853-35

Query Match 100.0%; Score 41; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
| | | | |
Db 3 GHRPLDK 9

RESULT 13
US-08-472-535-9
; Sequence 9, Application US/08472535
; Patent No. 5711931
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lees, Robert S.
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/472,535
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5711931nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
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; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Picollinoyl
; OTHER INFORMATION: /note= "The amino terminal residue is
; OTHER INFORMATION: pyridine-2-carboxyl; the thiol of the cysteine
; OTHER INFORMATION: residue is protected by an acetamidomethyl
; US-08-472-535-9

Query Match 100.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
| | | | |
Db 4 GHRPLDK 10

RESULT 14
US-08-484-774-9
; Sequence 9, Application US/08484774
; Patent No. 5807538
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Lees, Robert S.
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/484,774
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5807538nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= Picollinoyl
; OTHER INFORMATION: /note= "The amino terminal residue is
; OTHER INFORMATION: pyridine-2-carboxyl; the thiol of the cysteine
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OTHER INFORMATION: residue is protected by an acetoamidomethyl

US-08-484-774-9

Query Match 100.0%; Score 41; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.054; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 4 GHRPLDK 10

RESULT 15

US-08-266-178A-9
 ; Sequence 9, Application US/08266178A
 ; Patent No. 6017510
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Richard T
 ; APPLICANT: Buttram, Scott
 ; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 ; TITLE OF INVENTION: Imaging Inflammation
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Banner & Allegretti, Ltd.
 ; STREET: 10 South Wacker Drive, Suite 3000
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/266,178A
 FILING DATE: 27-JUN-1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: No. 6017510nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 92,112

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 FEATURE:

NAME/KEY: Modified-site
 LOCATION: 1..3
 OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= The amino terminal residue is
 pyridine-2-carbonyl; the thiol of the cysteine
 residue is protected by an acetoamidomethyl

US-08-266-178A-9

Query Match 100.0%; Score 41; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.054; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 Db 4 GHRPLDK 10

Search completed: June 16, 2003, 16:05:29
 Job time : 11.2667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:00:28 ; Search time 32 Seconds
(without alignments)
33.313 Million cell updates/sec

Title: US-09-424-940A-2

Perfect score: 50

Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

ID	Score	Query Match	Length	ID	Description
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2	50	100.0	8	14	AAR44837
3	50	100.0	8	15	AAR63270
4	50	100.0	8	15	AAR65793
5	41	82.0	7	8	AAP71314
6	41	82.0	7	11	AAR05558
7	41	82.0	7	15	AAR63269
8	41	82.0	7	15	AAR65792
9	41	82.0	7	22	ABE76979
10	41	82.0	10	16	AAW11931

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	8	9	AAP82686
2	50	100.0	8	14	AAR44837
3	50	100.0	8	15	AAR63270
4	50	100.0	8	15	AAR65793
5	41	82.0	7	8	AAP71314
6	41	82.0	7	11	AAR05558
7	41	82.0	7	15	AAR63269
8	41	82.0	7	15	AAR65792
9	41	82.0	7	22	ABE76979
10	41	82.0	10	16	AAW11931

11	41	82.0	12	13	AAR28629
12	41	82.0	12	14	AAR44829
13	41	82.0	12	14	AAR44838
14	41	82.0	16	14	AAR44830
15	41	82.0	28	14	AAR40010
16	41	82.0	29	14	AAR42547
17	41	82.0	30	14	AAR42546
18	41	82.0	30	14	AAR42546
19	41	82.0	118	21	AAG00151
20	41	82.0	140	22	AAU33273
21	41	82.0	141	22	AAO10778
22	41	82.0	150	21	AAG00150
23	41	82.0	453	22	AAW78493
24	41	82.0	491	16	AAR82243
25	41	82.0	491	22	AAW78492
26	41	82.0	495	22	AAW79475
27	41	82.0	495	22	AAW79476
28	41	82.0	495	22	AAW79477
29	41	82.0	539	22	AAW78491
30	40	80.0	182	23	ABB93430
31	39	78.0	67	23	ABP34803
32	37	74.0	145	22	AAU40707
33	37	74.0	575	22	ABB60076
34	37	74.0	923	22	ABB59000
35	36	72.0	11	21	AAW10666
36	36	72.0	11	21	AAW10629
37	36	72.0	105	21	AAW1348
38	36	72.0	105	23	ABP31218
39	36	72.0	159	23	ABP30199
40	36	72.0	165	23	ABP27176
41	35	70.0	39	23	AAU91250
42	35	70.0	41	22	ABG08987
43	35	70.0	202	22	AAG71790
44	35	70.0	305	22	AAG71593
45	35	70.0	305	22	AAG72216

ALIGNMENTS

RESULT 1
AAP82686
ID AAP82686 standard; peptide: 8 AA.
AC AAP82686;
DT 05-DEC-1990 (first entry)
DE Human fibrin beta chain N-terminal.
KW Fibrin; beta chain; N-terminal; monoclonal antibody; thrombosis.
XX Synthetic.
XX JP63093800-A.
XX 25-APR-1988.
XX 08-OCT-1986; 86JP-0237876.
XX 08-OCT-1986; 86JP-0237876.
XX (MITN) MITSUBISHI GAS CHEM KK.
XX WPI; 1988-152086/22.
XX New anti-human fibrin monoclonal antibody for diagnosing thrombosis
PT - prepd. from hybridoma obtd. by applying cell fusion mouse spleen
PT and mouse myeloma cells, and measures human fibrin.
XX Claim 1; Page 1; 8pp; Japanese.
XX The peptide is linked to a carrier protein via a linking agent and
CC

N-terminal human f
Human fibrin beta-
Human fibrin beta-
Human fibrin beta-
Scintigraph imagin
Leukocyte-binding
Leukocyte-binding
Human beta-fibrino
Human secreted pro
Novel human secret
Human polypeptide
Human secreted pro
Human protein SEQ
Human fibrinogen B
Human protein SEQ
Human protein SEQ
Human protein SEQ
Human protein SEQ
Human protein SEQ
Herbicide daily activ
Human ORF3776 prot
Propionibacterium
Drosophila melanog
Fibrinogen-beta pe
Fibrinogen-beta c
Human ORF ORF1112
Human ORF191 prote
Streptococcus poly
Streptococcus poly
Mouse homologue of
Novel human diagno
Human olfactory re
Human olfactory re
Human olfactory re

CC used to immunise mice. The mouse spleen cells and amveloma cell
 CC line can be fused to produce a hybridoma secreting MAb's which bind
 CC specifically to human fibrin but not fibrinogen.

XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 50; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDKC 8
 DB 1 GHRPLDKC 8
 |||||

RESULT 2
 AAR44837
 ID AAR44837 standard; peptide; 8 AA.
 XX
 AC AAR44837;
 XX
 DT 20-JUN-1994 (first entry)
 XX Human fibrin beta-chain N-terminal peptide A.
 DE
 XX Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 XX
 OS Synthetic.
 XX
 PN JP05304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX WPI; 1993-408334/51.
 DR Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 XX having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 PT
 PS Example 1; Page 14; 38pp; Japanese.
 XX
 CC Human fibrin beta-chain peptides A and B were synthesised and coupled
 CC to BSA for injection into mice. The peptides were used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
 CC are used in the production of bispecific monoclonal antibodies
 CC which also recognise truncated tPA mutants lacking the finger, EGF and
 CC Kringle 1 domains.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 50; DB 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDKC 8
 DB 1 GHRPLDKC 8
 |||||

RESULT 3
 AAR63270
 ID AAR63270 standard; peptide; 8 AA.
 XX
 AC AAR63270;
 XX

DT 21-JUL-1995 (first entry)
 DE Synthetic beta-peptide used to raise monoclonal antibody 59D8.
 XX
 KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
 KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
 KW coronary stent implantation; adjunctive therapy; fibrinogen;
 KW haemorrhage.
 XX
 OS Synthetic.
 XX
 PN W09425491-A.
 XX
 PD 10-NOV-1994.
 XX
 PF 03-MAY-1994; 94WO-US04881.
 XX
 PR 03-MAY-1993; 93US-0058699.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (UYEM-) UNIV EMORY.
 XX
 PI Bode C, Haber E, Runge M;
 XX
 DR WPI; 1994-358195/44.
 XX
 XX Fibrin-binding antibody linked to thrombin inhibitor - useful for
 PT preventing blood coagulation by specifically targeting inhibitor
 PT to site of thrombin activity
 PT
 XX Example 1; Page 14; 53pp; English.
 PS
 XX This sequence represents a synthetic beta-peptide which was used to
 CC immunopurify the monoclonal antibody 59D8 which was raised against
 CC beta-peptide (see also AAR63269). The antibody binds fibrin and may be
 CC used in the chimeric molecule of the invention. The chimeric molecule
 CC further comprises a thrombin inhibitor linked to the fibrin-binding
 CC antibody through a covalent linkage. The chimeric molecule allows
 CC fibrin-specific antibody targeting of hirudin and other thrombin
 CC inhibitors, which is more potent than thrombin on its own. The epitope
 CC to which 59D8 binds becomes available only after thrombin cleaves
 CC fibrinopeptide B. The chimeric protein may be used for preventing
 CC coagulation of the blood. Anti-thrombin targeting can be esp. useful
 CC in highly thrombogenic situations such as coronary stent implantation
 CC and can be used as an adjunctive therapy with highly selective
 CC thrombolytic agents. The thrombin inhibitor is localised to sites
 CC of thrombin activity by the antibody which binds to thrombin but does
 CC not cross react with uncleaved fibrinogen. The selectivity of
 CC inhibition allows the total amount of thrombin inhibitor used to be
 CC substantially reduced, resulting in a reduced potential for generalised
 CC haemorrhaging.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 50; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDKC 8
 DB 1 GHRPLDKC 8
 |||||

RESULT 4
 AAR65793
 ID AAR65793 standard; peptide; 8 AA.
 XX
 AC AAR65793;
 XX
 DT 26-JUN-1995 (first entry)
 XX
 DE Fibrin-specific epitopic peptide.
 XX

KW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
 KW antifibrin-specific monoclonal antibodies.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 8

FT /note= "May be absent and if present
 FT may be bonded to keyhole limpet
 FT hemocyanin."

XX US5357042-A.

XX PN 18-OCT-1994.

XX PD 23-APR-1984; 84US-0603155.

XX PR 23-APR-1984; 84US-0603155.

XX PR 30-JAN-1986; 84US-0824228.

XX PR 22-DEC-1989; 89US-0454954.

XX PR 24-AUG-1992; 92US-0932729.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PI Haber E, Hui K, Matsueda GR;

XX XN WPI; 1994-332411/41.

XX XN Synthetic epitopic peptide(s) of variable length - capable of
 PT eliciting fibrin specific antibodies free of fibrinogen
 PT cross-reactivity.

XX XN Claim 3; Column 18; 12pp; English.

XX XN AAR65789-R65794 are synthetic peptides comprising fibrin-specific
 CC epitopic sequences, they can be used to prepare hybridoma cell
 CC lines, which produce antifibrin-specific monoclonal antibodies
 CC substantially devoid of fibrinogen cross-reactivity. These
 CC antibodies are useful in the in vivo and in vitro detection
 CC of thrombi and fibrin deposits.

XX XN Query Match 100.0%; Score 50; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8

DB 1 GHRPLDKC 8

RESULT 5

AAP71314

ID AAP71314 standard; peptide; 7 AA.

XX AC AAP71314;

XX XN 03-OCT-2002 (updated)

DT 19-JUN-1991 (first entry)

XX DE Sequence of fibrin immunogen for the prepn. of monoclonal antibodies
 DE (MABs).

XX XN Fibrin-specific monoclonal antibody; screening.

XX XN Homo sapiens.

XX XN Key Location/Qualifiers

FT Misc-difference 7

FT /label= Lys-OH

XX XN WO8706263-A.

XX PD 22-OCT-1987.

XX XX 14-APR-1987; 87WO-US00862.

XX XX 14-APR-1986; 86US-0851514.

XX XX (GEHO-) GEN HOSPITAL CORP.

XX XX (GENO-) GEN HOSPITAL CORP.

XX XX Matsueda GR, Haber E;

XX XN WPI; 1987-306855/43.

XX XN Screening of fibrin-specific monoclonal antibodies - by contact
 PT with immobilised crosslinked fibrin clot and screening with
 PT detectable labelling step

XX XN Disclosure; Page 7; 41pp; English.

XX XN The MABs are specific to fibrin without fibrinogen cross-reactivity.
 CC They have increased binding to in vitro and in vivo thrombi. The
 CC MABs can be used in immunoassays for fibrin in the presence of
 CC fibrinogen or other proteins. They can be used as immunoaffinity
 CC ligands for the purification of fibrin.
 CC (Updated on 03-OCT-2002 to add missing OS field.)

XX XN Query Match 82.0%; Score 41; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

DB 1 GHRPLDK 7

RESULT 6

AAR05558

ID AAR05558 standard; peptide; 7 AA.

XX AC AAR05558;

XX XN 11-OCT-1990 (first entry)

DT Peptide antigenic to fibrin.

XX XN fibrin; fibrinogen; thrombi; immunoaffinity.

XX XN Synthetic.

XX XN Key Location/Qualifiers

FT Misc-difference 2 /label=His or Pro

FT Misc-difference 4 /label=Pro or Val

FT Misc-difference 5 /label=Leu or Val

FT Misc-difference 6 /label=Asp or Glu

FT Misc-difference 7 /label=Lys or Arg

XX XN US4927916-A.

XX XN 22-MAY-1990.

XX XN 30-JAN-1986; 86US-0824228.

XX XN 23-APR-1984; 84US-0603155.

XX XN 30-JAN-1986; 86US-0824228.

(GEHO-) GEN HOSPITAL CORP.
 PI Matsueda GR, Haber E, Hui K;
 DR WPI; 1990-185723/24.
 XX Fibrin-specific monoclonal antibodies -
 PT lacking fibrinogen cross-reactivity, obtd. using peptide(s)
 PT comprising fibrin-specific epitopic sequences.
 XX
 PS Claim 1; Page 17; 12pp; English.
 XX
 CC Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be
 CC raised without cross-reactivity to fibrinogen. They are
 CC particularly useful in detection of fibrin and thrombi.
 XX
 SQ Sequence 7 AA;
 Query Match 82.0%; Score 41; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GHRPLDK 7
 Db 1 GHRPLDK 7
 RESULT 7
 AAR63269
 ID AAR63269 standard; peptide; 7 AA.
 AC AAR63269;
 XX
 XX 21-JUL-1995 (first entry)
 DT
 DE Beta-peptide used to raise monoclonal antibody 59D8.
 DE
 XX Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
 KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
 KW coronary stent implantation; adjunctive therapy; fibrinogen;
 KW haemorrhage.
 XX
 OS Synthetic.
 XX
 XX WO9425491-A.
 PN
 XX 10-NOV-1994.
 PD
 XX 03-MAY-1994; 94WO-US04881.
 PF
 XX 03-MAY-1993; 93US-0058699.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA (UYEM-) UNIV EMORY.
 XX
 PI Bode C, Haber E, Runge M;
 XX
 DR WPI; 1994-358195/44.
 XX
 PT Fibrin-binding antibody linked to thrombin inhibitor - useful for
 PT preventing blood coagulation by specifically targeting inhibitor
 PT to site of thrombin activity
 XX
 PS Example 1; Page 13; 53pp; English.
 XX
 CC This sequence represents beta-peptide which was used to raise the
 CC monoclonal antibody 59D8. The antibody binds fibrin and may be used
 CC in the chimeric molecule of the invention. The chimeric molecule
 CC further comprises a thrombin inhibitor linked to the fibrin-binding
 CC antibody through a covalent linkage. The chimeric molecule allows
 CC fibrin-specific antibody targeting of hirudin and other thrombin
 CC inhibitors, which is more potent than thrombin on its own. The epitope
 CC to which 59D8 binds becomes available only after thrombin cleaves

fibrinopeptide B. The chimeric protein may be used for preventing
 CC coagulation of the blood. Anti-thrombin targeting can be esp. useful
 CC in highly thrombogenic situations such as coronary stent implantation
 CC and can be used as an adjunctive therapy with highly selective
 CC thrombolytic agents. The thrombin inhibitor is localised to sites
 CC of thrombin activity by the antibody which binds to thrombin but does
 CC not cross react with uncleaved fibrinogen. The selectivity of
 CC inhibition allows the total amount of thrombin inhibitor used to be
 CC substantially reduced, resulting in a reduced potential for generalised
 CC haemorrhaging.
 XX
 SQ Sequence 7 AA;
 Query Match 82.0%; Score 41; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GHRPLDK 7
 Db 1 GHRPLDK 7
 RESULT 8
 AAR65792
 ID AAR65792 standard; peptide; 7 AA.
 XX
 AC AAR65792;
 XX
 XX 26-JUN-1995 (first entry)
 DT
 DE Fibrin-specific epitopic peptide.
 DE
 XX Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
 KW antifibrin-specific monoclonal antibodies.
 KW
 XX Synthetic.
 OS
 XX US5357042-A.
 PN
 XX 18-OCT-1994.
 PD
 XX 23-APR-1984; 84US-0603155.
 PF
 XX 23-APR-1984; 84US-0603155.
 PR
 XX 30-JAN-1986; 86US-0824228.
 PR
 XX 22-DEC-1989; 89US-0454954.
 PR
 XX 24-AUG-1992; 92US-0932729.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 XX Haber E, Hui K, Matsueda GR;
 PI
 XX WPI; 1994-332411/41.
 DR
 XX Synthetic epitopic peptide(s) of variable length - capable of
 PT eliciting fibrin specific antibodies free of fibrinogen
 PT cross-reactivity.
 PT
 XX Claim 2; Column 18; 12pp; English.
 PS
 XX AAR65789-R65794 are synthetic peptides comprising fibrin-specific
 CC epitopic sequences, they can be used to prepare hybridoma cell
 CC lines, which produce antifibrin-specific monoclonal antibodies
 CC substantially devoid of fibrinogen cross-reactivity. These
 CC antibodies are useful in the in vivo and in vitro detection
 CC of thrombi and fibrin deposits.
 CC
 XX
 SQ Sequence 7 AA;
 Query Match 82.0%; Score 41; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 9
ABB76979
ID ABB76979 standard; peptide; 9 AA.
XX
AC ABB76979;
XX
XX 22-JUL-2002 (first entry)
XX
XX Residues 45-54 of human fibrinogen beta chain precursor.
XX
XX Anti-arthritis; anti-inflammatory; fibrin; rheumatoid polyarthritis;
KW human; fibrinogen beta chain.
XX
XX Homo sapiens.
XX
XX FR2795735-A1.
XX
XX 05-JAN-2001.
XX
XX 01-JUL-1999; 99FR-0008470.
XX
XX 01-JUL-1999; 99FR-0008470.
XX
XX (UYTO-) UNIV TOULOUSE SABATIER PAUL.
XX
XX Serre G, Sebbag M;
XX
XX WPI; 2001-114394/13.
XX
XX New citrulline-containing polypeptide from fibrin, useful for diagnosis
PT and treatment of rheumatoid polyarthritis
XX
XX Example 1; Page 12; 23pp; French.
XX
XX The present invention relates to a citrulline (Cit) containing
CC polypeptide derived from all or part of the alpha- or beta-chains of
CC fibrin by substitution of at least one arginine residue by Cit. The Cit
CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
CC therapeutically for neutralising the RP-associated autoimmune response.
CC The present sequence is a fragment (residues 45-54) of the human
CC fibrinogen beta chain precursor, which was used in an example from the
CC invention.
XX
XX Sequence 9 AA;
SQ
Query Match 82.0%; Score 41; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 10
AAW11931
ID AAW11931 standard; peptide; 10 AA.
XX
AC AAW11931;
XX
XX 02-APR-1997 (first entry)
XX
XX Fibrinogen A-alpha-chain residues 17-26.
XX
XX Monoclonal; antibody; human; soluble; fibrin; fibrinogen;
KW urea-treated; des-AABB; A-alpha-chain; immunosassay; diagnosis;
KW disseminated intravascular coagulation.

QY 1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 11
AAR28629
ID AAR28629 standard; peptide; 12 AA.
XX
AC AAR28629;
XX
XX 22-MAR-1993 (first entry)
XX
XX N-terminal human fibrin peptide.
XX
XX bispecific hybrid monoclonal antibody; thrombolytic agent;
KW cardiac infarction; arterial embolism; cerebral infarction;
KW peripheral arterial/venous obstruction; retinal arterial obstruction.
XX
XX Homo sapiens.
XX
XX EP513778-A.
XX
XX 19-NOV-1992.
XX
XX 14-MAY-1992; 92EP-0108134.
XX
XX 17-MAY-1991; 91JP-0112874.
XX
XX 13-MAR-1992; 92JP-0055025.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Iwasa S, Kurokawa T, Watanabe A;
XX

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XX Homo sapiens.
XX
XX WO9512617-A1.
XX
XX 11-MAY-1995.
XX
XX 01-NOV-1994; 94WO-JP01844.
XX
XX 02-NOV-1993; 93JP-0297325.
XX
XX (IATR ) IATRON LAB INC.
XX
XX Inuzuka K, Ito Y, Kohno I, Soe G;
XX
XX WPI; 1995-206667/27.
XX
XX Monoclonal antibody reactive with soluble human fibrin - but not
PT with fibrinogen, is useful for fibrin immunoassay in plasma
PT specimens
XX
XX Example 3; Page 15; 32pp; Japanese.
XX
XX A novel monoclonal antibody (MAB) reacts with human soluble fibrin,
CC but not with human fibrinogen. Specifically when the MAB reacts
CC with urea-treated des-AABB fibrin the reaction is not inhibited by
CC peptides corresponding to fibrinogen A-alpha-chain residues 17-26
CC (AAW11931), B-beta-chain residues 15-24 (AAW11932) or gamma-chain
CC residues 312-324 (AAW11933). The MAB is useful in immunoassays for
CC soluble fibrin in plasma samples (e.g. by sandwich immunoassays)
CC particularly for the diagnosis of pathological conditions such as
CC disseminated intravascular coagulation.
XX
XX Sequence 10 AA;
SQ
Query Match 82.0%; Score 41; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 11
AAR28629
ID AAR28629 standard; peptide; 12 AA.
XX
AC AAR28629;
XX
XX 22-MAR-1993 (first entry)
XX
XX N-terminal human fibrin peptide.
XX
XX bispecific hybrid monoclonal antibody; thrombolytic agent;
KW cardiac infarction; arterial embolism; cerebral infarction;
KW peripheral arterial/venous obstruction; retinal arterial obstruction.
XX
XX Homo sapiens.
XX
XX EP513778-A.
XX
XX 19-NOV-1992.
XX
XX 14-MAY-1992; 92EP-0108134.
XX
XX 17-MAY-1991; 91JP-0112874.
XX
XX 13-MAR-1992; 92JP-0055025.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Iwasa S, Kurokawa T, Watanabe A;
XX

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DR WPI; 1992-383677/47.
 XX BI:specific antibody useful for treating thrombotic obstructive
 PT diseases e.g. cardiac infarction - comprises antithrombus
 PT antibody variable region and anti-thrombolytic substance antibody
 PT 3 variable region with no heavy chain constant region domains 2 and
 XX
 PS Disclosure; Page 3; 30pp; English.
 XX
 CC This sequence represents an N-terminal peptide of human fibrin. It
 CC was used in the production of bispecific monoclonal antibodies which
 CC are specific for fibrins, but do not bind fibrinogen, and are
 CC specific for anti-thrombolytic substance. The compsn. contg. these
 CC Abs lacks the side effects of prior art Ab targeted thrombolytic
 CC agents and has enhanced thrombolytic activity.
 XX
 SQ Sequence 12 AA;
 Query Match 82.0%; Score 41; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 1 GHRPLDK 7
 RESULT 12
 AAR44829
 ID AAR44829 standard; peptide; 12 AA.
 XX
 AC AAR44829;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Human fibrin beta-chain N-terminal peptide (1-11)-Cys.
 XX
 KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..11
 FT Modified-site 12 /note- "human fibrin beta-chain residues 1-11"
 FT /note- "BSA carrier is attached to Cys"
 XX
 PN JP05304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 WPI; 1993-408334/51.
 XX
 DR Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 XX having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 PT
 XX Disclosure; Page 9; 38pp; Japanese.
 XX
 CC Human fibrin beta-chain N-terminal peptide (1-11)-Cys was
 CC synthesised and coupled to BSA for injection into mice. The peptide
 CC was used to raise antibodies to human fibrin. Monoclonal antibodies
 CC specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins

CC lacking the finger, EGF and Kringle 1 domains.
 XX
 SQ Sequence 12 AA;
 Query Match 82.0%; Score 41; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 1 GHRPLDK 7
 RESULT 13
 AAR44838
 ID AAR44838 standard; peptide; 12 AA.
 XX
 AC AAR44838;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Human fibrin beta-chain peptide B.
 XX
 KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 OS Synthetic.
 XX
 PN JP05304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 WPI; 1993-408334/51.
 XX
 DR Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 XX having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 PT
 XX Example 1; Page 14; 38pp; Japanese.
 XX
 CC Human fibrin beta-chain peptides A and B were synthesised and coupled
 CC to BSA for injection into mice. The peptides were used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
 CC are used in the production of bispecific monoclonal antibodies
 CC which also recognise truncated tPA muteins lacking the finger, EGF and
 CC Kringle 1 domains.
 XX
 SQ Sequence 12 AA;
 Query Match 82.0%; Score 41; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 6 GHRPLDK 12
 RESULT 14
 AAR44830
 ID AAR44830 standard; peptide; 16 AA.
 XX
 AC AAR44830;
 XX
 DT 20-JUN-1994 (first entry)
 XX

DE Human fibrin beta-chain internal peptide fragment.
 XX
 KW Tissue plasminogen activator; t-PA; muten; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 XX
 OS Synthetic.
 XX
 PN JP05304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-408334/51.
 XX
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX
 PS Disclosure; Page 9; 38pp; Japanese.
 XX
 CC Human fibrin internal peptide fragment was identified as a
 CC candidate immunogen to raise antibodies to human fibrin. Monoclonal
 CC antibodies specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA mutelins
 CC lacking the finger, EGF and Kringle 1 domains.
 XX
 SQ Sequence 16 AA;
 Query Match 82.0%; Score 41; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 6 GHRPLDK 12
 RESULT 15
 AAR40010
 ID AAR40010 standard; peptide; 28 AA.
 XX
 AC AAR40010;
 XX
 DT 23-MAY-1994 (first entry)
 XX
 DE Scintigraph imaging agent specific binding peptide.
 XX
 KW Reagent; site imaging; technetium-99m labelled; peptide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 28
 FT /note- "C-terminal amide"
 XX
 PN W09321962-A.
 XX
 PD 11-NOV-1993.
 XX
 PF 19-APR-1993; 93WO-US03687.
 XX
 PR 30-APR-1992; 92US-0871282.
 XX
 PA (DIAT-) DIATECH INC.
 XX
 PI Buttram S, Civitello ER, Dean RT, Lister-James J, McBride W;
 XX

DR WPI; 1993-368429/46.
 XX
 PT Reagents for preparing scintigraphic imaging agents - contg.
 .PT technetium-99m labelled peptide(s) contg. 3-100 aminoacid(s)
 XX
 PS Claim 35; Page 39; 55pp; English.
 XX
 CC The sequence is that of a specific binding peptide used as part of
 CC a reagent for preparing a scintigraphic imaging agent for imaging
 CC sites within a mammalian body. In this the peptide is covalently
 CC linked to a radiolabel-binding moiety which is capable of forming
 CC a complex with a radioisotope, pref. technetium-99m.
 XX
 SQ Sequence 28 AA;
 Query Match 82.0%; Score 41; DB 14; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 1 GHRPLDK 7
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 Job time : 32 secs

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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:02:14 ; Search time 11.7333 Seconds
(without alignments)
20.061 Million cell updates/sec

Title: US-09-424-940A-2
Perfect score: 50
Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	8	1	US-08-058-699-11
2	41	82.0	7	1	US-08-058-699-10
3	41	82.0	10	2	US-08-448-547-1
4	41	82.0	28	1	US-08-486-135-12
5	41	82.0	28	1	US-08-470-152-12
6	41	82.0	28	2	US-08-468-964B-10
7	41	82.0	28	2	US-07-871-282A-10
8	41	82.0	28	2	US-08-290-853-33
9	41	82.0	28	2	US-08-253-678A-10
10	41	82.0	28	3	US-08-582-134B-10
11	41	82.0	30	3	US-08-170-299-10
12	41	82.0	30	2	US-08-290-853-35
13	41	82.0	31	1	US-08-472-535-9
14	41	82.0	31	1	US-08-484-774-9
15	41	82.0	31	3	US-08-266-178A-9
16	41	82.0	491	1	US-08-206-176-4
17	34	68.0	9	4	US-09-258-754-234
18	34	68.0	9	4	US-09-042-107-234
19	34	68.0	245	4	US-08-469-260A-38
20	34	68.0	378	2	US-09-055-097-1
21	33	66.0	353	2	US-08-758-621-6
22	33	66.0	353	4	US-09-107-858-6
23	32	64.0	20	1	US-08-644-456-4
24	32	64.0	2183	1	US-08-348-891A-7
25	32	64.0	2183	2	US-08-905-817-7
26	32	64.0	2763	3	US-08-496-944-2
27	31	62.0	56	4	US-09-177-249-296

28	31	62.0	170	1	US-08-227-372-1
29	31	62.0	170	6	5194425-3
30	31	62.0	215	1	US-08-107-684B-9
31	31	62.0	215	1	US-08-107-684B-13
32	31	62.0	219	4	US-09-134-001C-4644
33	31	62.0	450	3	US-09-120-365-68
34	31	62.0	450	4	US-09-515-039-68
35	30	60.0	21	1	US-08-507-124-4
36	30	60.0	117	4	US-09-199-637A-33
37	30	60.0	170	4	US-09-199-637A-158
38	30	60.0	253	4	US-09-180-109A-35
39	30	60.0	254	4	US-09-180-109A-31
40	30	60.0	259	3	US-08-906-769-190
41	30	60.0	259	3	US-08-906-616-190
42	30	60.0	259	4	US-08-639-075A-190
43	30	60.0	259	4	US-09-004-731-85
44	30	60.0	259	4	US-09-012-431-190
45	30	60.0	259	4	US-08-749-699-85

ALIGNMENTS

RESULT 1
US-08-058-699-11
; Sequence 11, Application US/08058699
; Patent No. 5443827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marschall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058.699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-058-699-11

Query Match 100.0%; Score 50; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
|||||
Db 1 GHRPLDKC 8

RESULT 2

US-08-058-699-10
; Sequence 10, Application US/08058699
; Patent No. 543827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marschall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Javis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 03433/004001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-058-699-10

Query Match 82.0%; Score 41; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKC 7
|||||
Db 1 GHRPLDKC 7

RESULT 3

US-08-448-547-1
; Sequence 1, Application US/08448547
; Patent No. 5821068
; GENERAL INFORMATION:
; APPLICANT: Soe, Gilbu
; APPLICANT: Kohno, Isao
; APPLICANT: Inuzuka, Kimiko
; APPLICANT: Ito, Yumiko
; TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
; TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,547
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01844
; FILING DATE: 01-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-297325
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-38931
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-448-547-1

Query Match 82.0%; Score 41; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKC 7
|||||
Db 1 GHRPLDKC 7

RESULT 4

US-08-486-135-12
; Sequence 12, Application US/08486135
; Patent No. 5720934
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,135

;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5720934nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,205-N
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-486-135-12

Query Match 82.0%; Score 41; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 5
US-08-470-152-12
; Sequence 12, Application US/08470152
; Patent No. 5780007
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging
; CORRESPONDENCE ADDRESS: 19
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5780007nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-152-12

Query Match 82.0%; Score 41; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 6
US-08-468-964B-10
; Sequence 10, Application US/08468964B
; Patent No. 5922303
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,964B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-964B-10

Query Match 82.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 7
US-07-871-282A-10
; Sequence 10, Application US/07871282A
; Patent No. 5965107
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for

;; TITLE OF INVENTION: Imaging
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Diatide, Inc.
;; STREET: 9 Delta Drive
;; CITY: Londonderry
;; STATE: NH
;; COUNTRY: USA
;; ZIP: 03053
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/871,282A
;; FILING DATE: 20-APR-1992
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDaniels, Patricia A.
;; REGISTRATION NUMBER: 33,194
;; REFERENCE/DOCKET NUMBER: DITI 111
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (603) 437-8970
;; TELEFAX: (603) 437-8977
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-07-871-282A-10

Query Match 82.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 8
US-08-290-853-33
; Sequence 33, Application US/08290853
; Patent No. 5989519
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,853
; FILING DATE: 11-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5989519nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112-H

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1
;; OTHER INFORMATION: /label= BAT
;; OTHER INFORMATION: /note= "The amino terminus is linked to a BAT
;; OTHER INFORMATION: radiolabel binding moiety."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 28
;; OTHER INFORMATION: /label= Amide
;; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
;; OTHER INFORMATION: amide"
US-08-290-853-33
Query Match 82.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7
RESULT 9
US-08-253-678A-10
; Sequence 10, Application US/08253678A
; Patent No. 5997844
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
; TITLE OF INVENTION: IMAGING
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,678A
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: DITI 112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (603) 437-8970
; TELEFAX: (603) 437-8977
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid

STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-253-678A-10

Query Match 82.0%; Score 41; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 10

US-08-582-134B-10
Sequence 10, Application US/08582134B
Patent No. 6074627

GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582.134B
FILING DATE: 14-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-582-134B-10

Query Match 82.0%; Score 41; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 11

US-08-170-299-10
Sequence 10, Application US/08170299
Patent No. 6086849
GENERAL INFORMATION:

APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,299
FILING DATE: 09-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 6086849nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,205-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-170-299-10

Query Match 82.0%; Score 41; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 12

US-08-290-853-35
Sequence 35, Application US/08290853
Patent No. 5989519
GENERAL INFORMATION:

APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,853

;; FILING DATE: 11-OCT-1994
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5989519nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,112-H
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 35:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1..3
;; OTHER INFORMATION: /label= Picolinoyl
;; OTHER INFORMATION: /note= "The amino terminal residue is
;; OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine is
;; OTHER INFORMATION: protected by an acetamidomethyl group."
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 30
;; OTHER INFORMATION: /label= Amide
;; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
;; OTHER INFORMATION: amide"
US-08-290-853-35

Query Match 82.0%; Score 41; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 GHRPLDK 7
 |||||
DB 3 GHRPLDK 9

RESULT 13
US-08-472-535-9
;; Sequence 9, Application US/08472535
;; Patent No. 5711931
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T
;; APPLICANT: Lees, Robert S.
;; APPLICANT: Buttram, Scott
;; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
;; TITLE OF INVENTION: Imaging Inflammation
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive, Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/472,535
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5711931nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,112-J
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000

;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1..3
;; OTHER INFORMATION: /label= Picolinoyl
;; OTHER INFORMATION: /note= "The amino terminal residue is
;; OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine
;; OTHER INFORMATION: residue is protected by an acetamidomethyl
US-08-472-535-9

Query Match 82.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 GHRPLDK 7
 |||||
DB 4 GHRPLDK 10

RESULT 14
US-08-484-774-9
;; Sequence 9, Application US/08484774
;; Patent No. 5807538
;; GENERAL INFORMATION:
;; APPLICANT: Dean, Richard T
;; APPLICANT: Lees, Robert S.
;; APPLICANT: Buttram, Scott
;; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
;; TITLE OF INVENTION: Imaging Inflammation
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Banner & Allegretti, Ltd.
;; STREET: 10 South Wacker Drive, Suite 3000
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,774
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5807538nan, Kevin E
;; REGISTRATION NUMBER: 35,303
;; REFERENCE/DOCKET NUMBER: 92,112-K
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; TELEX: 910-221-5317
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 1..3
;; OTHER INFORMATION: /label= Picolinoyl
;; OTHER INFORMATION: /note= "The amino terminal residue is
;; OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine

OTHER INFORMATION: residue is protected by an acetoamidomethyl
US-08-484-774-9

Query Match 82.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 4 GHRPLDK 10

RESULT 15
US-08-266-178A-9
; Sequence 9, Application US/08266178A
; Patent No. 6017510
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,178A
; FILING DATE: 27-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6017510nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..3
; OTHER INFORMATION: /label= picolinoyl
; OTHER INFORMATION: /note= "the amino terminal residue is
; OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine
; OTHER INFORMATION: residue is protected by an acetoamidomethyl
US-08-266-178A-9

Query Match 82.0%; Score 41; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 4 GHRPLDK 10

Search completed: June 16, 2003, 16:05:30
Job time : 12.7333 secs

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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:01:49 ; Search time 13.3333 Seconds
(without alignments)
57.681 Million cell updates/sec

Title: US-09-424-940A-2

Perfect score: 50
Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73.*

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	82.0	31	2 A05297	fibrinogen beta ch
2	41	82.0	491	1 FGHUB	fibrinogen beta ch
3	39	78.0	725	2 A86328	protein F18014.27
4	37	74.0	82	2 D82773	hypothetical prote
5	37	74.0	482	2 T15829	hypothetical prote
6	37	74.0	518	2 B84514	probable cytochrom
7	37	74.0	591	2 S73790	hypothetical prote
8	36	72.0	201	2 C95399	probable transcrip
9	36	72.0	240	2 A82632	hypothetical prote
10	36	72.0	468	1 F8E08	fibrinogen beta ch
11	36	72.0	1490	2 T47840	multi resistance p
12	35	70.0	463	2 A38463	fibrinogen beta ch
13	35	70.0	562	2 T27807	hypothetical prote
14	35	70.0	615	2 D96499	probable UDP-gluc
15	35	70.0	1071	2 T18307	suppressor protein
16	34	68.0	122	1 W1LAI	alpha-amylase/typ
17	34	68.0	130	1 TNLJGG	trans-activating t
18	34	68.0	130	2 S12157	trans-activating t
19	34	68.0	409	2 F90825	probable integrase
20	34	68.0	416	2 A85684	probable integrase
21	34	68.0	421	2 T29789	hypothetical prote
22	34	68.0	673	2 T40817	zinc finger protei
23	34	68.0	782	2 JC7284	phospholipase A2 (
24	34	68.0	795	2 A84608	hypothetical prote
25	34	68.0	911	2 T29134	hypothetical prote
26	34	68.0	1576	2 T03277	pol protein - yeas
27	33	66.0	225	2 A75550	Mut/nudix family
28	33	66.0	325	2 H95278	conserved hypothet
29	33	66.0	326	2 C98346	hypothetical prote

30	33	66.0	326	2 AD2936	polymerase epsilon
31	33	66.0	353	2 T52184	zinc transporter 2
32	33	66.0	427	2 G98259	methionine gamma-1
33	33	66.0	427	2 A83025	methionine gamma-1
34	33	66.0	485	2 AB0706	probable phoR prot
35	33	66.0	1058	2 D82654	ankyrin-like prote
36	33	66.0	1635	2 T14075	chitinase (EC 3.2
37	32	64.0	73	2 S45349	trans-activating t
38	32	64.0	116	2 T17674	hypothetical prote
39	32	64.0	189	2 E82256	conserved hypothet
40	32	64.0	296	2 B71305	hypothetical prote
41	32	64.0	309	2 S40749	hypothetical prote
42	32	64.0	372	2 H81291	hypothetical prote
43	32	64.0	374	2 F97257	glycosyltransferas
44	32	64.0	383	2 T23182	hypothetical prote
45	32	64.0	423	2 T20233	hypothetical prote

ALIGNMENTS

RESULT 1

A05297
fibrinogen beta chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996
C:Accession: B94308; A03123; A37512; A05297; B37512; D03118
R:Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A:Title: Studies of the structure of canine fibrinogen.
A:Reference number: A94308; MOID:76081726; PMID:1198547
A:Accession: B94308
A:Molecule type: protein
A:Residues: 1-31 <BIR>
R:Blomback, B.; Blomback, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A:Title: Studies on fibrinopeptides from mammals.
A:Reference number: A03118
A:Accession: A03123
A:Molecule type: protein
A:Residues: 1-19 <BLO>
R:Krajewski, T.; Blomback, B.
Acta Chem. Scand. 22, 1339-1346, 1968
A:Reference number: A37512; MOID:69066367; PMID:5727635
A:Accession: A37512
A:Molecule type: protein
A:Residues: 1-19 <KRA>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen di
F:1-19/Product: fibrinopeptide B #status experimental <APT>
F:2/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F:3/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 82.0%; Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GHRPLDK 7
Db	20	GHRPLDK 26

RESULT 2

FGHUB
fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000
C:Accession: B43568; A90469; B90469; A94433; A90437; A94309; G54223; A03121
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.

A:Reference number: A90041; MUID:84305751; PMID:6383194
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A:Title: Cloning of fibrinogen genes and their cDNA
A:Reference number: A90038; MUID:83254384; PMID:6575700
A:Contents: annotation
R:Kirschbaum, N.E.; Bdzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COO
A:Reference number: A37117; MUID:90337977; PMID:2143188
A:Contents: annotation; hementin cleavage site
A:Note: hementin, a protease from Haemateria ghilianii, the giant South American le
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cl
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-sta
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Genetics:
A:Gene: GDB:FGB
A:Cross-references: GDB:119130; OMIM:134830
A:Map position: 4q28-4q28
A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PII
ins are contained in the core. Two three-chain coiled coils emerge from this core an
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disul
C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutam
F:1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
F:31-491/Product: fibrinogen beta chain #status experimental <MAT>
F:31-44/Product: fibrinopeptide B #status experimental <APT>
F:45-491/Product: fibrin beta chain #status experimental <FGB>
F:45-47/Region: polymerization site
F:99-228/Domain: fibrinogen disulfide ring homology <FDR>
F:238-487/Domain: fibrinogen beta/gamma homology <FBG>
F:31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status exper
F:44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
F:95/Disulfide bonds: interchain (to alpha-55) #status experimental
F:106/Disulfide bonds: interchain (to alpha-68) #status experimental
F:110/Disulfide bonds: interchain (to gamma-45) #status experimental
F:223/Disulfide bonds: interchain (to alpha-184) #status experimental
F:227/Disulfide bonds: interchain (to gamma-161) #status experimental
F:231-316,241-270,424-437/Disulfide bonds: #status experimental
F:394/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 82.08; Score 41; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
|||||
Db 45 GHRPLDK 51

RESULT 3
A86328
protein F18014.27 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: A86328
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor
chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
Ansn, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis

A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A86328
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-725 <STO>
 A:Cross-references: GB:AE005172; NID:g8778424; PIDN:AAF79432.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: FL8014.27
 A:Map position: 1

Query Match 78.0%; Score 39; DB 2; Length 725;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
 ||| |||
 DB 555 GHKPDCK 562

RESULT 4

D82773
 hypothetical protein XF0702 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: D82773
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: D82773
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-82 <SIM>
 A:Cross-references: GB:AE003913; GB:AE003849; NID:g9105578; PIDN:AAF83512.1; GSPDB:GN00141
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fromm, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF0702

Query Match 74.0%; Score 37; DB 2; Length 82;
 Best Local Similarity 75.0%; Pred. No. 3.3;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
 ||| |||
 DB 59 GHSPLGKC 66

RESULT 5

T15829
 hypothetical protein C53C9.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
 C:Accession: T15829
 R:Bentley, D. submitted to the EMBL Data Library, June 1995
 A:Description: The sequence of C. elegans cosmid C53C9.
 A:Reference number: Z18413
 A:Accession: T15829

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-482 <BEN>
 A:Cross-references: EMBL:U28734; NID:g861255; PID:g1945480; PIDN:AAB52604.1; GSPDB: A:Experimental source: strain Bristol N2; clone C53C9
 C:Genetics:
 A:Gene: CESP:C53C9.3
 A:Map position: X
 A:Introns: 19/2; 49/3; 128/3; 189/2; 203/3; 254/3; 273/1; 311/2; 372/2; 449/1

Query Match 74.0%; Score 37; DB 2; Length 482;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
 ||||| |
 DB 155 HRPLDVC 161

RESULT 6

B84514
 probable cytochrome P450 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 23-Mar-2001
 C:Accession: B84514
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallo euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: B84514
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-518 <SPTO>
 A:Cross-references: GB:AE002093; NID:g4587680; PIDN:AAD25850.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g14100
 A:Map position: 2

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C:Keywords: heme; iron; metalloprotein
 F:453/Binding site: heme iron (Cys) (axial ligand) #status predicted
 Query Match 74.0%; Score 37; DB 2; Length 518;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
 ||| |||
 DB 112 GHPPIDEC 119

RESULT 7

S73790
 hypothetical protein A19_ORF591 - Mycoplasma pneumoniae (strain ATCC 29342)
 C:Species: Mycoplasma pneumoniae
 A:Variety: ATCC 29342
 C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
 C:Accession: S73790
 R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneum A:Reference number: S73327; MUID:97105885; PMID:8948633
 A:Accession: S73790

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-591 <HIM>

A:Cross-references: EMBL:AE000046; GB:U00089; NID:g1674152; PIDN:AA996112.1; PID:g1 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 19 C:Genetics:
 A:Genetic code: SGC3
 C:Superfamily: Mycoplasma pneumoniae hypothetical protein A19_ORF591

Query Match 74.0%; Score 37; DB 2; Length 591;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKC 8
 I I I I I I
 Db 240 GENPLDKC 247

RESULT 8

C95399
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C95399
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: C95399
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-201 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK65757.1; PID:g14524255; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSYMA
 R:Galibert, F.; Flinan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMA2008
 A:Genome: plasmid

Query Match 72.0%; Score 36; DB 2; Length 201;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 I I I I I I
 Db 175 GHRPLD 180

RESULT 9

AE2632
 C:Species: Agrobacterium tumefaciens (strain C58, Dupont)
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AE2632
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AE2632
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-240 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AAL41475.1; PID:g17738801; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu0456
 A:Map position: circular chromosome

Query Match 72.0%; Score 36; DB 2; Length 240;

Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
 I I I I I I
 Db 144 HRPLRKC 150

RESULT 10

FGBOB
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
 C:Accession: A03122; B03117; B37507; A37513; S02443
 R:Blomback, B.; Doolittle, R.F.
 Acta Chem. Scand. 17, 1816-1819, 1963
 A:Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide
 A:Reference number: A03122
 A:Accession: A03122
 A:Molecule type: protein
 A:Residues: 1-4 <BLQ>
 R:Sjoquist, J.; Blomback, B.; Wallen, P.
 Ark. Kemi 16, 425-436, 1960
 A:Title: Amino acid sequence of bovine fibrinopeptides.
 A:Reference number: A03117
 A:Accession: B03117
 A:Molecule type: protein
 A:Residues: 5-21 <SUQ>
 R:Martinielli, R.A.; Ingalls, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leac
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fib
 A:Reference number: A37507; MUID:79164394; PMID:434821
 A:Accession: B37507
 A:Molecule type: protein
 A:Residues: 22-53 <MAR>
 R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
 A:Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrin
 A:Reference number: A37513; MUID:81199473; PMID:6262803
 A:Accession: A37513
 A:Molecule type: mRNA
 A:Residues: 44-468 <CHU>
 R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
 FEBS Lett. 232, 56-60, 1988
 A:Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) lead
 A:Reference number: S02443; MUID:88211875; PMID:2966748
 A:Accession: S02443
 A:Molecule type: protein
 A:Residues: 373-374 <WED>
 C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopep
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen dis
 C:Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein
 F:76-205/Domain: fibrinogen disulfide ring homology <FDR>
 F:215-464/Domain: fibrinogen beta/gamma homology <FGB>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:6/Binding site: sulfate (Tyr) (covalent) #status experimental
 F:21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
 F:371/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 72.0%; Score 36; DB 1; Length 468;
 Best Local Similarity 85.7%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 I I I I I I
 Db 22 GHRPYDK 28

RESULT 11

T47840

multi resistance protein homolog - Arabidopsis thaliana
 N: Alternate names: protein T209.140
 C: Species: Arabidopsis thaliana (mouse-ear cress)
 C: Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
 C: Accession: T47840
 R: Nyakatura, G.; Fartmann, B.; Dauner, D.; Stert, W.; Holland, R.; Weichselgartner, M.; submitted to the Protein Sequence Database, February 2000
 A: Reference number: 224475
 A: Accession: T47840
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-1490 <NYA>
 A: Cross-references: EMBL:AL138658
 A: Experimental source: cultivar Columbia; BAC clone T209
 C: Genetics:
 A: Map position: 3
 A: Introns: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3; 1369/1; 1449/1
 A: Note: T209.140
 C: Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 72.0%; Score 36; DB 2; Length 1490;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 DB 1226 GHRPLD 1231

RESULT 12
 A38463
 fibrinogen beta chain - chicken (fragment)
 C: Species: Gallus gallus (chicken)
 C: Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
 C: Accession: A38463
 R: Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
 Biochemistry 30, 3290-3294, 1991
 A: Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage site
 A: Reference number: A38463; MUID: 91182745; PMID: 2009266
 A: Accession: A38463
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Residues: 1-463 <WEI>
 A: Cross-references: GB:M58514; NID: g2111779; PIDN: AAA48770.1; PID: g2111780
 C: Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 F: 73-202/Domain: fibrinogen disulfide ring homology <FDR>
 F: 212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 70.0%; Score 35; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
 DB 19 HRPLDK 24

RESULT 13
 T27807
 hypothetical protein ZK265.1 - Caenorhabditis elegans
 C: Species: Caenorhabditis elegans
 C: Date: 13-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C: Accession: T27807
 R: Dobson, R.
 submitted to the EMBL Data Library, October 1996
 A: Reference number: Z20422
 A: Accession: T27807
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-562 <WIL>
 A: Cross-references: EMBL: Z61143; PIDN: CAB03514.1; GSPDB: GN00019; CESP: ZK265.1
 A: Experimental source: clone ZK265
 C: Genetics:

A: Gene: CESP: ZK265.1
 A: Map position: 1
 A: Introns: 19/2; 46/3; 93/2; 219/2; 274/3; 319/2; 362/3; 431/3; 482/1

Query Match 70.0%; Score 35; DB 2; Length 562;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
 DB 404 GYRPIDYC 411

RESULT 14
 D96499
 probable UDP-glucose,sterol glucosyltransferase [imported] - Arabidopsis thaliana
 C: Species: Arabidopsis thaliana (mouse-ear cress)
 C: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C: Accession: D96499
 R: Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A: Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A: Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A: Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A: Reference number: A86141; MUID: 21016719; PMID: 11130712
 A: Accession: D96499
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-615 <STO>
 A: Cross-references: GB: AE005173; NID: g5080759; PIDN: AAD39269.1; GSPDB: GN00141
 C: Genetics:
 A: Gene: T10P12.7
 A: Map position: 1

Query Match 70.0%; Score 35; DB 2; Length 615;
 Best Local Similarity 75.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
 DB 48 GHRGLDHC 55

RESULT 15
 T18307
 suppressor protein - yeast (Kluyveromyces marxianus var. lactis)
 C: Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
 C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C: Accession: T18307
 R: Groom, K.R.; Heyman, H.C.; Steffen, M.C.; Hawkins, L.; Martin, N.C.
 Yeast 14, 77-87, 1998
 A: Title: Kluyveromyces lactis SEF1 and its Saccharomyces cerevisiae homologue bypas
 A: Reference number: Z13599; MUID: 98144791; PMID: 9483797
 A: Accession: T18307
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 1-1071 <GRO>
 A: Cross-references: EMBL: U92898; NID: g2104692; PID: g2104693; PIDN: AAC39353.1
 C: Genetics:
 A: Gene: SEF1
 C: Superfamily: unassigned GAL4-type zinc cluster proteins; GAL4 zinc binuclear clus
 F: 81-121/Domain: GAL4 zinc binuclear cluster homology <GL4>

Query Match 70.0%; Score 35; DB 2; Length 1071;
 Best Local Similarity 62.5%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDK 8

Db |111: |
 79 GHREVTSC 86

Search completed: June 16, 2003, 16:05:02
Job time : 14.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:00:53 ; Search time 6.93333 Seconds
(without alignments)
47.857 Million cell updates/sec

Title: US-09-424-940A-2
Perfect score: 50
Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	82.0	31	1 FIBB CANFA	P02677 canis famil
2	41	82.0	491	1 FIBB HUMAN	P02675 homo sapien
3	37	74.0	591	1 YD72 MYCPN	P75409 mycoplasma
4	36	72.0	468	1 FIBB BOVIN	P02676 bos taurus
5	35	70.0	463	1 FIBB CHICK	Q02020 gallus gall
6	35	70.0	479	1 FIBB RAT	P14480 rattus norv
7	35	70.0	1071	1 SEF1 KLULA	P87164 kluyveromyc
8	34	68.0	122	1 IAAT_ELECO	P01087 eleusine co
9	34	68.0	130	1 TAT_HV2BE	P18098 human immun
10	34	68.0	130	1 TAT_HV2D1	P17759 human immun
11	34	68.0	130	1 TAT_HV2G1	P18044 human immun
12	33	66.0	895	1 DSC3 MOUSE	P55850 mus musculu
13	33	66.0	1581	1 LMG3 MOUSE	Q9r0B6 mus musculu
14	32	64.0	94	1 TAT_SIVAI	Q02838 simian immu
15	32	64.0	275	1 SLBP_MOUSE	P97440 mus musculu
16	32	64.0	288	1 YL87_CAEEL	P34445 caenorhabdi
17	32	64.0	296	1 Y608_TREPA	O83617 treponema p
18	32	64.0	475	1 YM61_YEAST	Q03652 saccharomyc
19	32	64.0	560	1 EFS_MOUSE	O64355 mus musculu
20	32	64.0	698	1 YMCA_ECOLI	P75882 escherichia
21	32	64.0	785	1 SOK2_YEAST	P53438 saccharomyc
22	32	64.0	883	1 HMDH_XENLA	P20715 xenopus lae
23	32	64.0	1080	1 HDA4_CHICK	P83038 gallus gall
24	32	64.0	1084	1 HDA4_HUMAN	P56524 homo sapien
25	32	64.0	1295	1 GLP1_CAEEL	P13508 caenorhabdi
26	32	64.0	2183	1 RRPL_MEASA	P35975 measles vir
27	32	64.0	2183	1 RRPL_MEASE	P12576 measles vir
28	32	64.0	5217	1 HTSI_COCCA	Q01886 cochlidiobol
29	31	62.0	119	1 RM14_TETPY	P10850 tetrahymena
30	31	62.0	168	1 MBP_RABIT	P25274 oryctolagus
31	31	62.0	169	1 MBP_BOVIN	P02687 bos taurus
32	31	62.0	170	1 MFAS_BOVIN	Q28022 bos taurus
33	31	62.0	215	1 PCP_BACSU	P28618 bacillus su

34	31	62.0	225	1 NRFC_HAEIN	P45015 haemophilus
35	31	62.0	333	1 TRAW_ZYMMO	Q9teq9 zymomonas m
36	31	62.0	363	1 TRMA_PSEFL	Q9rns9 pseudomonas
37	31	62.0	374	1 TGT_SYNY3	Q55983 synechocyst
38	31	62.0	391	1 YT73_CAEEL	Q11087 caenorhabdi
39	31	62.0	424	1 THC2_METTH	O27617 methanobact
40	31	62.0	450	1 CYSP_TRYBB	P14658 trypanosoma
41	31	62.0	633	1 IPAA_SHIFL	P18010 shigella fl
42	31	62.0	649	1 HS7C_ICTPU	P47773 ictalurus p
43	31	62.0	1077	1 UBPS_HUMAN	Q96ru2 homo sapien
44	31	62.0	1587	1 LMG3_HUMAN	Q9y6n6 homo sapien
45	31	62.0	1648	1 RRPO_CGMVS	P15523 cucumber gr

ALIGNMENTS

RESULT 1
FIBB_CANFA STANDARD; PRT; 31 AA.
AC P02677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=76081726; PubMed=1198547;
RA Birken S., Wilner G.D., Canfield R.E.;
RT "Studies of the structure of canine fibrinogen.";
RL Thromb. Res. 7:599-610(1975).
RN [2]
RP SEQUENCE OF 1-19.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [3]
RP SEQUENCE OF 1-19.
RX MEDLINE=69066367; PubMed=5727635;
RA Krajewski T., Blomback B.;
RT "The location of tyrosine-O-sulphate in fibrinopeptides.";
RL Acta Chem. Scand. 22:1339-1346(1968).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; A03123; A03123.
CC PIR; A05297; A05297.
CC InterPro: IPR002181; Fibrinogen_C.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
CC Blood coagulation; Plasma; Sulfation.
KW PEPTIDE 1 19 FIBRINOPEPTIDE B.
FT CHAIN 20 >31 FIBRINOGEN BETA CHAIN.
FT MOD_RES 2 2 SULFATION (IN B[2] CHAIN).
FT MOD_RES 3 3 SULFATION (IN B[1] & B[2] CHAINS).
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3731 MW; A043727257698156 CRC64;

Query Match 82.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

Db 11111111
20 GHRLDK 26

RESULT 2

ID FIBB_HUMAN STANDARD; PRT; 491 AA.

AC P02675;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].

GN FGB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-91344740; PubMed-2102623;

RA Chung D.W., Harris J.E., Davie E.W.;

RT "Nucleotide sequences of the three genes coding for human

RL fibrinogen.";

RL Adv. Exp. Med. Biol. 281:39-48(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-83283433; PubMed-6688356;

RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;

RT "Characterization of complementary deoxyribonucleic acid and genomic

RL deoxyribonucleic acid for the beta chain of human fibrinogen.";

RL Biochemistry 22:3244-3250(1983).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE-79124640; PubMed-420779;

RA Watt K.W.K., Takagi T., Doolittle R.F.;

RT "Amino acid sequence of the beta chain of human fibrinogen.";

RL Biochemistry 18:68-76(1979).

RN [7]

RP SEQUENCE OF 31-491.

RX MEDLINE-79124640; PubMed-420779;

RA Watt K.W.K., Takagi T., Doolittle R.F.;

RT "Amino acid sequence of the beta chain of human fibrinogen.";

RL Biochemistry 18:68-76(1979).

RN [7]

RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.

RX MEDLINE-76225080; PubMed-936108;

RA Blomback B., Hessel B., Hogg D.;

RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";

RL Thromb. Res. 8:639-658(1976).

RN [8]

RP SEQUENCE OF 1-38 FROM N.A.

RX MEDLINE-87146483; PubMed-3029722;

RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.;

RT Marguerie G.;

RT "Characterization of the 5'-flanking region for the human fibrinogen

RL beta gene.";

RL Nucleic Acids Res. 15:1615-1625(1987).

RN [9]

RP SEQUENCE OF 31-44.

RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;

RT "Studies on fibrinopeptides from primates.";

RL Acta Chem. Scand. 19:1788-1789(1965).

RN [10]

RP REVIEW, AND DISULFIDE BONDS.

RX MEDLINE-83254370; PubMed-6575689;

RA Henschen A., Lottspeich F., Kehl M., Southan C.;

RT "Covalent structure of fibrinogen.";

RL Ann. N.Y. Acad. Sci. 408:28-43(1983).

RN [11]

RP DISULFIDE BONDS.

RX MEDLINE-77245999; PubMed-891553;

RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;

RT "Primary structure of human fibrinogen. Characterization of

RL disulfide-containing cyanogen-bromide fragments.";

RL Eur. J. Biochem. 77:595-610(1977).

RN [12]

RP DISULFIDE BONDS.

RX MEDLINE-77245999; PubMed-891553;

RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.;

RA Casman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;

RT "The structures of fibrinogen and fibrin.";

RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K.;

RL Neurath H. (eds.);

RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,

RL Pergamon Press, New York (1978).

RN [13]

RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.

RX MEDLINE-84303751; PubMed-6383194;

RA Doolittle R.F.;

RT "Fibrinogen and fibrin.";

RL Annu. Rev. Biochem. 53:195-229(1984).

RN [14]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.

RX MEDLINE-97472408; PubMed-9333233;

RA Spraggon G., Everse S.J., Doolittle R.F.;

RT "Crystal structures of fragment D from human fibrinogen and its

RL crosslinked counterpart from fibrin.";

RL Nature 389:455-462(1997).

RN [15]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.

RX MEDLINE-98292395; PubMed-9628725;

RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;

RT "Crystal structure of fragment double-D from human fibrin with two

RL different bound ligands.";

RL Biochemistry 37:8637-8642(1998).

RN [16]

RP X-RAY CRYSTALLOGRAPHY.

RX MEDLINE-99175089; PubMed-10074346;

RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;

RT "Conformational changes in fragments D and double-D from human

RL fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";

RL Biochemistry 38:2941-2946(1999).

RN [17]

RP VARIANT BALTIMORE-2.

RX MEDLINE-89058942; PubMed-3194892;

RA Schmeizel C.H., Ebert R.F., Bell W.R.;

RT "A polymorphism at B beta 448 of fibrinogen identified during

RL structural studies of fibrinogen Baltimore II.";

RL Thromb. Res. 52:173-177(1988).

RN [18]

RP VARIANT ISE.

RX MEDLINE-91208409; PubMed-2018836;

RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.;

RA Asakura S., Shirakawa S.;

RT "A new congenital abnormal fibrinogen Ise characterized by the

RL replacement of B beta glycine-15 by cysteine.";

RL Blood 77:1958-1963(1991).

RN [19]

RP VARIANT NAPLES.

RX MEDLINE-92340664; PubMed-1634610;

RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;

```

RT RT "Molecular basis of fibrinogen Naples associated with defective
RT thrombin binding and thrombophilia. Homozygous substitution of B beta
RT 68 Ala-->Thr.;"
RL J. Clin. Invest. 90:238-244(1992).
RN [20]
RP VARIANTS IGMUIDEN AND NIJMEGEN.
RX MEDLINE-92228809; PubMed-1565641;
RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
RA Kerst A.F.J.A., Lord S.T.;
RT "Abnormal fibrinogens Igmuiden (B beta Arg14-->Cys) and Nijmegen (B
RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
RT complexes.;"
RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
RN [21]
RP VARIANT NEW YORK-1.
RX MEDLINE-85157605; PubMed-3156856;
RA Liu C.Y., Koehn J.A., Morgan F.J.;
RT "Characterization of fibrinogen New York 1. A dysfunctional
RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
RT exon 2 of the gene.;"
RL J. Biol. Chem. 260:4390-4396(1985).
CC -|- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -|- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
CC ENDS OF THE ALPHA CHAINS.
CC -|- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
CC -|- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -|- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC
CC EMBL; J00129; AAA52429.1; -
CC EMBL; J00131; AAA98115.1; -
CC EMBL; J00130; AAA98115.1; JOINED.
CC EMBL; J00132; AAA98116.1; -
CC EMBL; J00133; -; NOT_ANNOTATED_CDS.
CC EMBL; AF388026; AAK62470.1; -
CC EMBL; X05018; CAA28674.1; -
CC EMBL; M41983; AAA18024.2; -
CC EMBL; M26877; AAA52445.1; -
CC EMBL; M26876; AAA52445.1; JOINED.
CC
CC Query Match 82.0%; Score 41; DB 1; Length 491;
CC Best Local Similarity 100.0%; Pred. NO. 1.1;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 GHRPLDK 7
CC DB 45 GHRPLDK 51
CC
CC RESULT 3
CC YD72_MYCPN
CC ID YD72_MYCPN STANDARD; PRT; 591 AA.

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AC P75409;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MPN372 (A19_orf591).
GN MPN372 OR MP464.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 29342 / M129;
RX MEDLINE-97105885; PubMed-8948633;
RA Himmelreich R., Hilbert H., Flagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.;"
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC
CC EMBL; AE000046; AAB96112.1; -
CC InterPro; IPR003898; Borpert_toxa.
CC Pfam; PF02917; Pertussis_S1; 1.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 591 AA; 68057 MW; 5958C85C9EE29E90 CRC64;
CC
CC Query Match 74.0%; Score 37; DB 1; Length 591;
CC Best Local Similarity 75.0%; Pred. NO. 8.6;
CC Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 1 GHRPLDK 8
CC DB 240 GENPLDK 247
CC
CC RESULT 4
CC FIBB_BOVIN
CC ID FIBB_BOVIN STANDARD; PRT; 468 AA.
CC AC P02676;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN FGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 1-4.
RA Blomback B., Doolittle R.F.;
RT "The sequence of amino acids at the N-terminal end of bovine
RT fibrinopeptide B.;"
RL Acta Chem. Scand. 17:1816-1819(1963).
RN [2]
RP SEQUENCE OF 5-21.
RA Sjoquist J., Blomback B., Wallen P.;
RT "Amino acid sequence of bovine fibrinopeptides.;"
RL Ark. Kemi 16:425-436(1960).
RN [3]
RP SEQUENCE OF 22-53.
RX MEDLINE-79164394; PubMed-434821;
RA Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;
RT "Amino acid sequences of portions of the alpha and beta chains of

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RT bovine fibrinogen."
RL Arch. Biochem. Biophys. 192:27-32(1979).
RN [4]
RP SEQUENCE OF 44-468 FROM N.A.
RX MEDLINE=8119473; PubMed=6262803;
RA Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
RT "Characterization of a cDNA clone coding for the beta chain of bovine
RL fibrinogen."
RL Proc Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: V00110; CAA23444.1;
DR PIR: A03122; FGBOB.
DR HSP: P02675; IFZAF.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
FT PEPTIDE 1 21 FIBRINOPEPTIDE B.
FT CHAIN 22 468 FIBRINOGEN BETA CHAIN.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 6 6 SULFATION.
FT SITE 21 22 CLEAVAGE (BY THROMBIN; RELEASE
FT FIBRINOPEPTIDE B).
FT DISULFID 72 72 INTERCHAIN (WITH ALPHA).
FT DISULFID 83 83 INTERCHAIN (WITH ALPHA).
FT DISULFID 87 87 INTERCHAIN (WITH ALPHA).
FT DISULFID 200 200 INTERCHAIN (WITH ALPHA).
FT DISULFID 204 204 INTERCHAIN (WITH ALPHA).
FT DISULFID 208 293 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 401 414 BY SIMILARITY.
FT CARBOHYD 371 371 N-LINKED (GLCNAC... ) (PROBABLE).
SQ SEQUENCE 468 AA; 53340 MW; 2DED42F443AA4B37 CRC64;

Query Match 72.0%; Score 36; DB 1; Length 468;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 22 GHRPYDK 28
|||||

RESULT 5
FIBB_CHICK STANDARD; PRT; 463 AA.
AC Q02020;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
DN (Fragment).
GN FGB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE=91182745; PubMed=2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
RL cleavage site."
RL Biochemistry 30:3290-3294(1991).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL: M58514; AAA48770.1;
DR PIR: A38463; A38463.
DR HSP: P02675; IFZF.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
FT PEPTIDE 1 17 FIBRINOPEPTIDE B.
FT CHAIN 18 463 FIBRINOGEN BETA CHAIN.
FT MOD_RES 5 5 SULFATION (BY SIMILARITY).
FT SITE 17 18 CLEAVAGE (BY THROMBIN; RELEASE
FT FIBRINOPEPTIDE B).
FT DISULFID 69 69 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 84 84 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 197 197 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 201 201 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 205 289 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 397 410 BY SIMILARITY.
FT CARBOHYD 367 367 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 463 AA; 52678 MW; 2044CD49BA79EC7B CRC64;

Query Match 70.0%; Score 35; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
DB 19 HRPLDK 24
|||||

RESULT 6

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ID FIBR_RAT STANDARD; PRT; 479 AA.
 AC P14480;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN FGB.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95143386; PubMed=7841303;
 RA Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.;
 RT "Cloning of the complete coding sequence of rat fibrinogen B beta
 chain cDNA; interspecies conservation of fibrin beta 15-42 primary
 structure.";
 RL Blood Coagul. Fibrinolysis 5:487-496(1994).
 RN [2]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX MEDLINE=84194000; PubMed=6232608;
 RA Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
 RT "Potential basis for regulation of the coordinately expressed
 fibrinogen genes: homology in the 5' flanking regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
 RN [3]
 RP SEQUENCE OF 19-32.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [4]
 RP SEQUENCE OF 183-479 FROM N.A.
 RX MEDLINE=89378771; PubMed=2673932;
 RA Eastman E.M., Gilula N.B.;
 RT "Cloning and characterization of a cDNA for the B beta chain of rat
 fibrinogen: evolutionary conservation of translated and
 3'-untranslated sequences.";
 RL Gene 79:151-158(1989).
 RN [5]
 RP SEQUENCE OF 425-479 FROM N.A.
 RC STRAIN-Wistar; TISSUE=Liver;
 RX MEDLINE=87134033; PubMed=3817019;
 RA Sobczak J., Lotti A.-M., Taroux P., Duquet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 liver regeneration.";
 RL Exp. Cell Res. 189:47-56(1987).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U05675; AAA64866.1; -
 DR EMBL; M27220; AAA41160.1; -
 DR EMBL; K01336; AAA98625.1; -
 DR EMBL; M35602; AAA41159.1; -
 DR PIR; A05299; A05299.

DR PIR; PE0010; PE0010.
 DR HSP; P02675; IFZE.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KW Blood coagulation; Plasma; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.
 FT PEPTIDE 19 32 FIBRINOPEPTIDE B.
 FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
 FT (BY SIMILARITY).
 FT INTERCHAIN (WITH THE GAMMA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 215 215
 FT DISULFID 219 304
 FT DISULFID 229 258
 FT DISULFID 412 425
 FT CARBOHYD 382 382
 FT CONFLICT 28 30 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 439 439 LSI -> ILS (IN REF. 3).
 FT CONFLICT 441 441 L -> Q (IN REF. 5).
 FT CONFLICT 445 445 S -> T (IN REF. 5).
 FT CONFLICT 467 467 S -> A (IN REF. 5).
 FT CONFLICT 475 475 R -> K (IN REF. 5).
 FT CONFLICT 475 475 V -> F (IN REF. 5).
 SQ SEQUENCE 479 AA; 54303 MW; EC8C6DB77C3E0EC0 CRC64;
 Query Match 70.0%; Score 35; DB 1; Length 479;
 Best Local Similarity 71.4%; Pred. No. 17;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 Db 33 GHRPVD 39
 RESULT 7
 SEFI_KLUOLA STANDARD; PRT; 1071 AA.
 ID SEFI_KLUOLA
 AC P87164;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Suppressor protein SEFI.
 GN SEFI.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98144791; PubMed=9483797;
 RA Groom K.R., Heyman H.C., Steffen M.C., Hawkins L., Martin N.C.;
 RT "Kluyveromyces lactis SEFI and its Saccharomycetes cerevisiae homologue
 bypass the unknown essential function, but not the mitochondrial
 Rnae P function, of the S. cerevisiae RPM2 gene.";
 RL Yeast 14:77-87(1998).
 CC -1- FUNCTION: NOT KNOWN. SUPPRESSES THE LETHAL PHENOTYPE OF RPM2
 DELETION.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
 CLUSTER DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U02898; AAC39353.1; -
 DR InterPro: IPR001136; Fungl_Tn.
 DR Pfam; PF001172; Zn_c1us; 1.
 DR

DR SMART: SM00066; GAL4; 1.
 DR PROSITE: PS00463; ZN2_CYS6_FUNGAL_1; 1.
 DR PROSITE: PS00463; ZN2_CYS6_FUNGAL_2; 1.
 DR TRANSSCRIPTION REGULATION; DNA-BINDING; Nuclear protein; Zinc;
 KW Metal-binding.
 FT DNA_BIND 86 116 ZN(2)-CYS(6), FUNGAL-TYPE.
 SQ SEQUENCE 1071 AA; 120031 MW; 92CB05A3F703FB53 CRC64;
 Query Match 70.0%; Score 35; DB 1; Length 1071;
 Best Local Similarity 62.5%; Pred. No. 40;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GHRPLDKC 8
 DB 79 GHRPVTSC 86
 RESULT 8
 ID IANT_ELECO STANDARD; PRT; 122 AA.
 AC P01087;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-amylase/trypsin inhibitor (RBI) (RATI).
 OS Eleusine coracana (Indian finger millet) (Ragi).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Chloridoideae; Poaceae; Eleusine.
 OX NCBI_TaxID=4511;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Campos F.A.P., Richardson M.;
 RT "The complete amino acid sequence of the bifunctional alpha-
 amylase/trypsin inhibitor from seeds of ragi (Indian finger millet,
 Eleusine coracana Gaertn.)";
 RL FEBS Lett. 152:300-304 (1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC TISSUE=Seed;
 RA Strobl S., Maskos K., Wiegand G., Huber R., Gomis-Ruth F.X.,
 RA Glockshuber R.;
 RT "A novel strategy for inhibition of alpha-amylases: yellow meal worm
 alpha-amylase in complex with the Ragi bifunctional inhibitor at 2.5-A
 resolution.";
 RL Structure 6:911-921 (1998).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RC TISSUE=Seed;
 RA MEDLINE=99190826; PubMed=10089391;
 RA Gourinath S., Srinivasan A., Singh T.P.;
 RT "Structure of the bifunctional inhibitor of trypsin and alpha-amylase
 from ragi seeds at 2.9-A resolution.";
 RL Acta Crystallogr. D 55:25-30 (1999).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RC TISSUE=Seed;
 RA MEDLINE=20180431; PubMed=10713515;
 RA Gourinath S., Alam N., Srinivasan A., Betzel C., Singh T.P.;
 RT "Structure of the bifunctional inhibitor of trypsin and alpha-amylase
 from ragi seeds at 2.2 A resolution.";
 RL Acta Crystallogr. D 56:287-293 (2000).
 RN [5]
 RP STRUCTURE BY NMR.
 RC TISSUE=Seed;
 RA MEDLINE=95322379; PubMed=7599120;
 RA Strobl S., Muehlhahn P., Bernstein R., Wiltseck R., Maskos K.,
 RA Wunderlich M., Huber R., Glockshuber R., Holak T.A.;
 RT "Determination of the three-dimensional structure of the bifunctional
 alpha-amylase/trypsin inhibitor from ragi seeds by NMR
 spectroscopy.";

RL Biochemistry 34:8281-8293 (1995).
 CC -!- FUNCTION: MAY PLAY A PROTECTIVE ROLE AGAINST ENDO- AND EXOGENOUS
 CC HYDROLYTIC ACTIVITIES IN THE RAGI SEEDS.
 CC -!- TISSUE SPECIFICITY: SEEDS.
 CC -!- SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INHIBITOR
 CC FAMILY.
 DR PIR: A01326; WILAI.
 DR PDB: 1BIP; 10-JUL-95.
 DR PDB: 1BIU; 02-DEC-98.
 DR PDB: 1TMQ; 02-MAR-99.
 DR PDB: 1BIU; 08-MAR-00.
 DR InterPro: IPR003612; AAI.
 DR InterPro: IPR001768; Try/amyl inhtr.
 DR Pfam: PF00234; tryp_alpha_aml; 1.
 DR PRINTS: PR00808; AMLASEINHTR.
 DR SMART: SM00499; AAI; 1.
 DR PROSITE: PS00426; CEREAL_TRYP_AMYL_INH; 1.
 KW Serine protease inhibitor; Alpha-amylase inhibitor; 3D-structure.
 FT DISULFID 6 55
 FT DISULFID 20 44
 FT DISULFID 29 85
 FT DISULFID 45 103
 FT DISULFID 57 114
 FT VARIANT 25 26 ST -> AK.
 FT VARIANT 28 28 T -> A.
 FT VARIANT 70 70 P -> S.
 SQ SEQUENCE 122 AA; 13138 MW; C8ED7A01CD470E17 CRC64;
 Query Match 68.0%; Score 34; DB 1; Length 122;
 Best Local Similarity 71.4%; Pred. No. 6.8;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 HRPDLKC 8
 DB 14 HNPDLSC 20
 RESULT 9
 ID TAT_HV2BE STANDARD; PRT; 130 AA.
 AC P18098;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TAT protein (transactivating regulatory protein).
 GN TAT.
 OS Human immunodeficiency virus type 2 (isolate BEN) (HIV-2).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90281594; PubMed=2353457;
 RA Kirchhoff F., Jentsch K., Bachmann B., Stuke A., Laloux C.,
 RA Lueke W., Stahl-Henning C., Schneider J., Niesel K., Eigen M.,
 RA Hunsman G.;
 RT "A novel proviral clone of HIV-2: biological and phylogenetic
 relationship to other primate immunodeficiency viruses.";
 RL Virology 177:305-311 (1990).
 CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
 CC -!- MISCELLANEOUS: THIS ISOLATE IS FROM A GERMAN AIDS PATIENT (WITH
 CC PREDOMINANTLY NEUROLOGICAL COMPLICATIONS) WHO WAS PROBABLY
 CC INFECTED IN MALI.
 CC -----
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CC -----

DR EMBL; M30502; AAB00741.1; -;
DR HIV; M30502; TAT\$2BEN.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
AIDS.

SQ SEQUENCE 130 AA; 14463 MW; 5227D62952F8A625 CRC64;
Query Match 68.0%; Score 34; DB 1; Length 130;
Best Local Similarity 71.4%; Pred. No. 7.2;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 HRPLDKC 8
||||: |
Db 44 HRPLEPC 50

RESULT 10
TAT_HV2D1
ID TAT_HV2D1 STANDARD; PRT; 130 AA.
AC P17759;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tat protein (Transactivating regulatory protein).
GN TAT.

OS Human immunodeficiency virus type 2 (isolate D194) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11173;
X

RP SEQUENCE FROM N.A.
RX MEDLINE=89184631; PubMed=2467304;
RA Kuehn H., Kreutz R., Ruebsamen-Waigmann H.;
RA Biesert L., Kreutz R., Immlmann A., Henco K., Weichsner C.;
RA Andreesen R., Gelderblom H., Ruebsamen-Waigmann H.;
RT "Molecular cloning of two west African human immunodeficiency virus
type 2 isolates that replicate well in macrophages: a Gambian
isolate, from a patient with neurologic acquired immunodeficiency
syndrome, and a highly divergent Ghanaian isolate.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:2383-2387(1989).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=91045094; PubMed=2235509;
RA Kuehn H., Kreutz R., Ruebsamen-Waigmann H.;
RT "Nucleotide sequence of HIV-2D194, an isolate from a Gambian case of
'neuro-AIDS', which showed excellent growth in macrophages.";
RL Nucleic Acids Res. 18:6142-6142(1990).
CC -|- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -|- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -|- MISCELLANEOUS: THIS ISOLATE IS FROM A GAMBIAN CASE OF
CC 'NEURO-AIDS'.

CC -----
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CC EMBL; J04542; AAT76845.1; -;
CC EMBL; X52223; CAA36469.1; -;
DR HIV; J04542; TAT\$2D194.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.

DR PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
AIDS.

SQ SEQUENCE 130 AA; 14597 MW; 1A659CB2F933C537 CRC64;
Query Match 68.0%; Score 34; DB 1; Length 130;
Best Local Similarity 71.4%; Pred. No. 7.2;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 HRPLDKC 8
||||: |
Db 44 HRPLEAC 50

RESULT 11
TAT_HV2G1
ID TAT_HV2G1 STANDARD; PRT; 130 AA.
AC P18044;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tat protein (Transactivating regulatory protein).
GN TAT.

OS Human immunodeficiency virus type 2 (isolate Ghana-1) (HIV-2).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11171;
X

RP SEQUENCE FROM N.A.
RX MEDLINE=90122350; PubMed=2611042;
RA Hasegawa A., Tsujimoto H., Maki N., Ishikawa K.I., Miura T.,
RA Fukasawa M., Miki K., Hayami M.;
RT "Genomic divergence of HIV-2 from Ghana.";
RL AIDS Res. Hum. Retroviruses 5:593-604(1989).
CC -|- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.

CC -|- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -----
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CC EMBL; M30895; AAA43929.1; -;
DR PIR; JS0332; TNLJGG.
DR HIV; M30895; TAT\$2GH1.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
AIDS.

SQ SEQUENCE 130 AA; 14580 MW; 95F308B537027D67 CRC64;
Query Match 68.0%; Score 34; DB 1; Length 130;
Best Local Similarity 71.4%; Pred. No. 7.2;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 HRPLDKC 8
||||: |
Db 44 HRPLEAC 50

RESULT 12
DSC3_MOUSE
ID DSC3_MOUSE STANDARD; PRT; 895 AA.
AC P55850; O55122; O55110;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Desmocollin 3 precursor.
GN DSC3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=98049324; PubMed=9389456;
RA Chidgey M.A.J., Yue K.K.M., Gould S., Byrne C., Garrod D.R.;
RT "Changing pattern of desmocollin 3 expression accompanies epidermal
RL organisation during skin development.";
RL Dev. Dyn. 210:315-327(1997).
RN [2]
RP SEQUENCE OF 709-874 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
RP SPECIFICITY.
RX MEDLINE=98067789; PubMed=9404003;
RA King I.A., Angst B.D., Hunt D.M., Kruger M., Arnemann J., Buxton R.S.;
RT "Hierarchical expression of desmosomal cadherins during stratified
RN epithelial morphogenesis in the mouse.";
RL Differentiation 62:83-96(1997).
CC -1- FUNCTION: COMPONENT OF INTERCELLULAR DESMOsome JUNCTIONS. INVOLVED
CC IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
CC MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL
CC POSITIONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
CC ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 3A (SHOWN HERE) AND 3B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: FIRST EXPRESSED AT E13.0 IN EPITHELIUM OF
CC WHISKER PADS AND EXTERNAL NARES. AND IN MOST MATURE VIBRISSE
CC FOLLICLES. 12 HOURS LATER, PROMINENTLY EXPRESSED IN WHISKERS AND
CC DEVELOPING NAILS AND TEETH AND, AT LOW LEVELS, IN VENTRAL AND
CC LATERAL SKIN. AT E15.5, HIGHLY EXPRESSED IN GENERAL BODY EPIDERMIS
CC AND AT E16.5, DETECTED OVER ENTIRE EMBRYO. IN THE ADULT, HIGHLY
CC EXPRESSED IN BASAL LAYERS OF STRATIFIED CELLS.
CC -1- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
CC (POTENTIAL).
CC -1- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y11169; CA72045.1; -;
DR EMBL; AJ000329; CAA03996.1; -;
DR HSSP; P15116; INCJ.
DR MGD; MG1:119493; Dsc3.
DR InterPro; IPR002126; Cadherin.
DR InterPro; IPR000233; Cadherin_C_term.
DR Pfam; PF00028; cadherin; 5.
DR Pfam; PF01049; Cadherin_C_term; 1.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 5.
DR PROSITE; PS00232; CADHERIN.1; 3.
DR PROSITE; PS0268; CADHERIN.2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
KW Cytoskeleton; Calcium-binding; Alternative splicing.
FT SIGNAL 1 31
FT PROPEP 32 135
FT CHAIN 136 895
FT DOMAIN 136 695
FT TRANSNEM 696 716
FT DOMAIN 717 895
FT DOMAIN 136 243
FT DOMAIN 244 355
FT DOMAIN 356 472

FT DOMAIN 473 580
FT DOMAIN 581 691
FT CARBOHYD 166 166
FT CARBOHYD 392 392
FT CARBOHYD 547 547
FT CARBOHYD 630 630
FT VARSPLIC 831 838
FT VARSPLIC 839 895
FT CONFLICT 715 715
FT CONFLICT 750 767
FT CONFLICT 840 840
FT CONFLICT 873 874
FT SEQUENCE 895 AA; 100653 MW; D561E67C57232270 CRC64;
SQ SEQUENCE 895 AA; 100653 MW; D561E67C57232270 CRC64;
Query Match 66.0%; Score 33; DB 1; Length 895;
Best Local Similarity 62.5%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GHRPLDKC 8
DB 784 GHQTLDS 791
RESULT 13
LMG3_MOUSE
ID LMG3_MOUSE STANDARD; PRT; 1581 AA..
AC O9ROB6; Q9WTW6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Laminin gamma-3 chain precursor (Laminin 12 gamma 3).
GN LAMC3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Albus A.M., Burgeson B., Champlaud M.-F., Koch M., Olson P.;
RT "Mouse laminin 12 gamma 3 chain.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-1526 FROM N.A.
RX MEDLINE=99253969; PubMed=10318827;
RA Iivanainen A., Morita T., Tryggvason K.;
RT "Molecular cloning and tissue-specific expression of a novel murine
RT laminin gamma3 chain.";
RL J. Biol. Chem. 274:14107-14111(1999).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration, and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end.
CC THE GAMMA-3 CHAIN IS A SUBUNIT OF LAMININ-12.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Strongly expressed in capillaries and
CC arterioles of kidney as well as in interstitial Leydig cells of
CC testis.
CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -1- DOMAIN: DOMAIN IV IS GLOBULAR.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 11 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC -----
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CC EMBL; AF083372; AAF08983.1;
CC HSSP; P02468; 1KLO.
CC MGD; MGI:1344394; Lamc3.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR001886; LamNT.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC Pfam; PF00052; laminin_B; 1.
CC Pfam; PF00053; laminin_EGF; 10.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC ProDom; PD002082; LamNT; 1.
CC SMART; SM00180; EGF_Lam; 10.
CC SMART; SM00281; LamB; 1.
CC SMART; SM00136; LamNT; 1.
CC PROSITE; PS00022; EGF_1; UNKNOWN_8.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 28
FT CHAIN 29 1581
FT DOMAIN 29 279 LAMININ GAMMA-3 CHAIN.
FT DOMAIN 280 335 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 336 391 LAMININ EGF-LIKE 1.
FT DOMAIN 392 438 LAMININ EGF-LIKE 2.
FT DOMAIN 439 488 LAMININ EGF-LIKE 3.
FT DOMAIN 489 498 LAMININ EGF-LIKE 4.
FT DOMAIN 499 684 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 685 718 LAMININ EGF-LIKE 6.
FT DOMAIN 719 766 LAMININ EGF-LIKE 7.
FT DOMAIN 767 821 LAMININ EGF-LIKE 8.
FT DOMAIN 822 877 LAMININ EGF-LIKE 9.
FT DOMAIN 878 927 LAMININ EGF-LIKE 10.
FT DOMAIN 928 1024 LAMININ EGF-LIKE 11.
FT DOMAIN 1025 1581 DOMAIN II AND I.
FT DOMAIN 1029 1046 COILED COIL (POTENTIAL).
FT DOMAIN 1112 1153 COILED COIL (POTENTIAL).
FT DOMAIN 1208 1231 COILED COIL (POTENTIAL).
FT DOMAIN 1438 1468 COILED COIL (POTENTIAL).
FT DOMAIN 1510 1575 COILED COIL (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 640 640 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 849 849 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 991 991 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1162 1162 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1196 1196 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1320 1320 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1514 1514 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 9 9 L -> F (IN REF. 2).
FT CONFLICT 190 190 P -> T (IN REF. 2).
FT CONFLICT 195 195 R -> K (IN REF. 2).
FT CONFLICT 221 221 G -> S (IN REF. 2).
FT CONFLICT 394 394 C -> R (IN REF. 2).
FT CONFLICT 471 471 C -> Y (IN REF. 2).
FT CONFLICT 1150 1150 L -> LDEPQLFSLLK (IN REF. 2).
FT CONFLICT 1387 1387 H -> Q (IN REF. 2).
FT CONFLICT 1438 1439 AS -> TI (IN REF. 2).
FT CONFLICT 1479 1479 V -> I (IN REF. 2).
SQ SEQUENCE 1581 AA; 172316 MW; 51DFAD1F95E6AE81 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 1581;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 3 RPLDKC 8
DB 870 RPVDC 875

RESULT 14
TAT_SIVAI
ID TAT_SIVAI STANDARD; PRT; 94 AA.
AC Q02838;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Simian immunodeficiency virus (isolate AGM / clone GRI-1) (SIV-AGM).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=31684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91220680; PubMed=2024476;
RA Fomsgaard A., Hirsch V.M., Allan J.S., Johnson P.R.;
RT "A highly divergent proviral DNA clone of SIV from a distinct species
of African green monkey.";
RL Virology 182:397-402(1991).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
TRANS-ACTIVATING RESPONSE SEQUENCE (TAR) RNA ELEMENT AND
ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
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EMBL; M66437; AAA91926.3; .
DR EMBL; M58410; .; NOT_ANNOTATED_CDS.
DR InterPro; IPR001831; HIV_Tat.
DR Pfam; PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW AIDS.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
AIDS.
SQ SEQUENCE 94 AA; 10875 MW; D23ADFDC8B2A0D96 CRC64;

Query Match 64.0%; Score 32; DB 1; Length 94;
Best Local Similarity 71.4%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
DB 15 HRPLQPC 21

RESULT 15
SLBP_MOUSE
ID SLBP_MOUSE STANDARD; PRT; 275 AA.
AC P97440;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histone RNA hairpin-binding protein (Histone stem-loop binding
protein).
DE HBP OR SLBP.
GN HBP OR SLBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;


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RN SEQUENCE FROM N.A.
RP STRAIN=NIH Swiss; TISSUE=Embryo;
RX MEDLINE=97115884; PubMed=8957003;
RA Wang Z.-F., Whitfield M.L., Ingledue T.C. III, Dominski Z.,
RT Marzluff W.F.;
RT "The protein that binds the 3' end of histone mRNA: a novel
RT RNA-binding protein required for histone pre-mRNA processing.";
RL Genes Dev. 10:3028-3040(1996).
CC -1- FUNCTION: BINDS THE STEM-LOOP STRUCTURE OF REPLICATION-DEPENDENT
CC HISTONE PRE-MRNAs AND CONTRIBUTES TO EFFICIENT 3' END PROCESSING
CC BY STABILIZING THE COMPLEX BETWEEN HISTONE PRE-MRNA AND U7 SMALL
CC NUCLEAR RIBONUCLEOPROTEIN (SNRNP). COULD PLAY AN IMPORTANT ROLE IN
CC TARGETING MATURE HISTONE mRNA FROM THE NUCLEUS TO THE CYTOPLASM
CC AND TO THE TRANSLATION MACHINERY. STABILIZES MATURE HISTONE mRNA
CC AND COULD BE INVOLVED IN CELL-CYCLE REGULATION OF HISTONE GENE
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC (POLYRIBOSOME-
CC ASSOCIATED).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE SLBP FAMILY.
CC -----
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CC -----
DR EMBL; U75680; AAC53530.1; -.
DR MGD; MGI:108402; Slbp.
KW RNA-binding; mRNA processing; Nuclear protein; Phosphorylation.
FT MOD_RES 62 PHOSPHORYLATION (BY CDC2) (BY
FT SIMILARITY).
FT DOMAIN 129 198 RNA-BINDING (BY SIMILARITY).
SQ SEQUENCE 275 AA; 31603 MW; 538459F001C59AF4 CRC64;
Query Match 64.0%; Score 32; DB 1; Length 275;
Best Local Similarity 50.0%; Pred. NO. 39;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GHRPLDKC 8
Db |||:|:|
65 GHKPRSRC 72

```

Search completed: June 16, 2003, 16:03:35
Job time : 7.93333 secs

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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:01:29 ; Search time 25.6 Seconds
(without alignments)
64.390 Million cell updates/sec

Title: US-09-424-940A-2
Perfect score: 50
Sequence: 1 GHRPLDKC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriopl.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	84.0	377	12 Q99FX0	Q99fx0 human papil
2	41	82.0	411	4 Q8W77	Q8w77 homo sapien
3	40	80.0	182	10 Q9LFM1	Q9lfm1 arabidopsis
4	39	78.0	266	10 Q940Z1	Q940z1 arabidopsis
5	39	78.0	725	10 Q9LN43	Q9ln43 arabidopsis
6	39	78.0	3287	5 Q8T326	Q8t326 plasmodium
7	38	76.0	50	12 Q9E8G2	Q9e8g2 porcine ade
8	38	76.0	50	12 Q9E8F8	Q9e8f8 porcine ade
9	38	76.0	401	10 Q8RUP6	Q8rup6 oryza sativ
10	38	76.0	513	10 Q9AY56	Q9ay56 oryza sativ
11	37	74.0	82	16 Q9EFF7	Q9pf7 xylella fas
12	37	74.0	482	5 Q09937	Q09937 caenorhabdi
13	37	74.0	518	10 Q9SI49	Q9si49 arabidopsis
14	37	74.0	575	5 Q9G989	Q9g989 drosophila
15	37	74.0	923	5 Q9VA50	Q9va50 drosophila
16	36	72.0	201	16 Q92XY9	Q92xy9 rhizobium m

17	36	72.0	240	16 Q8UI44	Q8ui44 agrobacteri
18	36	72.0	246	11 Q8R328	Q8r328 mus musculu
19	36	72.0	385	11 Q9CS12	Q9cs12 mus musculu
20	36	72.0	415	10 Q9LDY0	Q9ldy0 arabidopsi
21	36	72.0	471	10 Q8SBA0	Q8sba0 oryza sativ
22	36	72.0	516	11 Q8R018	Q8r018 mus musculu
23	36	72.0	735	10 Q94E87	Q94e87 oryza sativ
24	36	72.0	800	10 Q8S213	Q8s213 oryza sativ
25	36	72.0	1490	10 Q9MIC7	Q9mic7 arabidopsi
26	35	70.0	505	4 Q9HA50	Q9ha50 homo sapien
27	35	70.0	562	5 Q94400	Q94400 caenorhabdi
28	35	70.0	615	10 Q9XIG1	Q9xig1 arabidopsi
29	35	70.0	838	10 Q9LSP8	Q9lsp8 arabidopsi
30	35	70.0	959	2 Q46583	Q46583 desulfovibr
31	35	70.0	1371	4 Q9Y2K2	Q9y2k2 homo sapien
32	34	68.0	130	15 P88145	P88145 human immun
33	34	68.0	258	12 Q9DKM4	Q9dkm4 spodoptera
34	34	68.0	292	4 Q9NUN2	Q9nun2 homo sapien
35	34	68.0	292	11 Q8VEC0	Q8vec0 mus musculu
36	34	68.0	370	11 Q920U9	Q920u9 mus musculu
37	34	68.0	370	11 Q920U8	Q920u8 mus musculu
38	34	68.0	370	11 Q920U7	Q920u7 mus spicile
39	34	68.0	370	11 Q91VC1	Q91vc1 mus musculu
40	34	68.0	371	11 Q88178	Q88178 rattus norv
41	34	68.0	371	11 Q920F0	Q920f0 mus musculu
42	34	68.0	373	12 Q9P296	Q9p296 pestivirus
43	34	68.0	378	4 Q96024	Q96024 homo sapien
44	34	68.0	380	4 Q95035	Q95035 homo sapien
45	34	68.0	416	16 Q8X775	Q8x775 escherichia

ALIGNMENTS

RESULT 1

Q99FX0 ID Q99FX0 PRELIMINARY; PRT; 377 AA.
AC Q99FX0
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative regulatory protein E2.
GN E2.
OS Human papillomavirus type 84.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=150546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066735; PubMed=11145894;
RA Terai M., Burk R.D.;
RT "Complete Nucleotide Sequence and Analysis of a Novel Human
Papillomavirus (HPV 84) Genome Cloned by an Overlapping PCR Method.";
RL Virology 279:109-115(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Burk R.D., Terai M.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EXBL: AF293960; AAK09274.1;
DR HSP: P17383; IDHM.
DR InterPro: IPR000427; E2_C.
DR InterPro: IPR001866; E2_N.
DR Pfam: PF00511; E2_C; 1.
DR Pfam: PF00508; E2_N; 1.
DR ProDom: PD000672; E2_C; 1.
DR ProDom: PD000678; E2_N; 1.
SQ SEQUENCE 377 AA; 43001 MW; 71FC5F656143A674 CRC64;

Query Match 84.0%; Score 42; DB 12; Length 377;
Best Local Similarity 75.0%; Pred. No. 2.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GHRPLDKC 8

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Db          265 GHRPVDSC 272
|||||
RESULT 2
ID Q8W777 PRELIMINARY; PRT; 411 AA.
AC Q8W777;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 46.9 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020762; AAR20762.1; -
DR InterPro; IPR002181; Fibrinogen_C.
DR InterPro; IPR001019; Gprotelin_alpha.
DR DR Pfam; PF00147; fibrinogen_C; 1.
DR DR Pfam; PF00503; G-alpha; 1.
DR DR SMART; SM00186; FBG; 1.
DR DR SMART; SM00275; G-alpha; 1.
KW Hypothetical protein.
SQ SEQUENCE 411 AA; 46884 MW; 601E4EA47F60E056 CRC64;

Query Match 82.0%; Score 41; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GHRPLDK 7
Db 45 GHRPLDK 51
|||||

RESULT 3
O9LFM1 PRELIMINARY; PRT; 182 AA.
AC Q9LFM1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical 20.6 kDa protein.
GN F211_250.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL360314; CAB96671.1; -
DR InterPro; IPR000719; Euk_pkinase.
DR ProDom; PD000001; Euk_pkinase; 1.
KW Hypothetical protein.
SQ SEQUENCE 182 AA; 20577 MW; F485F31EA802BEFC CRC64;

Query Match 80.0%; Score 40; DB 10; Length 182;
Best Local Similarity 75.0%; Pred. No. 3.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 GHRPLDK 8
Db 175 GHRPDKC 182
|||||

RESULT 4
O940Z1 PRELIMINARY; PRT; 266 AA.
ID Q940Z1;
AC Q940Z1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE At1g19520/F18014.36.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT Arabidopsis cdna clones;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT Arabidopsis ORF clones;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052347; AAK96539.1; -
DR EMBL; AY061908; AAL31235.1; -
DR InterPro; IPR002885; PPR.
DR Pfam; PF01535; PPR; 6.
DR TIGRFAMS; TIGR00756; PPR; 5.
SQ SEQUENCE 266 AA; 29615 MW; 46CB125C324A8A30 CRC64;

Query Match 78.0%; Score 39; DB 10; Length 266;
Best Local Similarity 75.0%; Pred. No. 6.9;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GHRPLDK 8
Db 96 GHRPDKC 103
|||||

RESULT 5
O9LN43 PRELIMINARY; PRT; 725 AA.
ID Q9LN43;
AC Q9LN43;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE F18014.27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

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RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F18014 from chromosome
 RT I.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC025808; AAF79432.1;
 DR InterPro: IPR002885; PPR.
 DR Pfam: PF01535; PPR; 8.
 DR TIGRFAMs: TIGR00756; PPR; 7.
 SQ SEQUENCE 725 AA; 82535 MW; 921B477745237EFA CRC64;

Query Match 78.0%; Score 39; DB 10; Length 725;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHRPLDKC 8
 II: I III
 Db 555 GHKPDKC 562

RESULT 6
 Q8T326 PRELIMINARY; PRT; 3287 AA.
 ID Q8T326
 AC Q8T326
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE PfEMP1 (Fragment).
 GN TM180VAR2.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TM180;
 RX MEDLINE=21927235; PubMed=11930336;
 RA Rowe J.A., Kyes S.A., Rogerson S.J., Babiker H.A., Raza A.;
 RT "Identification of a conserved Plasmodium falciparum var gene
 RT implicated in malaria in pregnancy.";
 RL J. Infect. Dis. 185:1207-1211(2002).
 DR EMBL: AJ420411; CAD20867.1;
 FT NON_TER 3287 3287
 SQ SEQUENCE 3287 AA; 383550 MW; 58F8F86FC244536 CRC64;

Query Match 78.0%; Score 39; DB 5; Length 3287;
 Best Local Similarity 85.7%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HRPLDKC 8
 I: IIIII
 Db 2872 HRLDKC 2878

RESULT 7
 Q9E8G2 PRELIMINARY; PRT; 50 AA.
 ID Q9E8G2
 AC Q9E8G2
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE ORF4.
 OS porcine adenovirus 5.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=45370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HNF-61;
 RX MEDLINE=20416365; PubMed=10958982;

RA Tuboly T., Nagy E.;
 RT "Sequence analysis and deletion of porcine adenovirus serotype 5 E3
 RT region.";
 RL Virus Res. 68:109-117(2000).
 DR EMBL: AF186621; AAG10229.1;
 SQ SEQUENCE 50 AA; 5521 MW; D546CCC59A16F417 CRC64;

Query Match 76.0%; Score 38; DB 12; Length 50;
 Best Local Similarity 85.7%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
 I: I I I I I
 Db 44 HRPLDTC 50

RESULT 8
 Q9E8F8 PRELIMINARY; PRT; 50 AA.
 ID Q9E8F8
 AC Q9E8F8
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE ORF4.
 OS porcine adenovirus 5.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=45370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HNF-70;
 RX MEDLINE=20416365; PubMed=10958982;
 RA Tuboly T., Nagy E.;
 RT "Sequence analysis and deletion of porcine adenovirus serotype 5 E3
 RT region.";
 RL Virus Res. 68:109-117(2000).
 DR EMBL: AF186622; AAG10234.1;
 SQ SEQUENCE 50 AA; 5589 MW; -02DDECC59A16F3F0 CRC64;

Query Match 76.0%; Score 38; DB 12; Length 50;
 Best Local Similarity 85.7%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
 I: I I I I I
 Db 44 HRPLDTC 50

RESULT 9
 Q8RUP6 PRELIMINARY; PRT; 401 AA.
 ID Q8RUP6
 AC Q8RUP6
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE P0703B11.15 protein (P0485B12.7 protein).
 GN P0703B11.15 OR P0485B12.7.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0703B11.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC


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RT clone:P0485B12.1;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003302; BAB85296.1; -
DR EMBL; AP003348; BAB86477.1; -
SQ SEQUENCE 401 AA; 46131 MW; 9BF7BA7748970E05 CRC64;

Query Match      76.0%; Score 38; DB 10; Length 401;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 120 GHSPLQKC 127

RESULT 10
Q9AY56 PRELIMINARY; PRT; 513 AA.
ID AC Q9AY56;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 57.9 kDa protein.
GN OSJNBA0027P10.13.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Craven B.,
RA Khalak H., Feldblum T.V., Quackenbush J., White O., Salzberg S.L.,
RA Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBA0027P10 genomic sequence.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084763; AAG60187.1; -
KW Hypothetical protein.
SQ SEQUENCE 513 AA; 57948 MW; C9EE96E9ABA816BB CRC64;

Query Match      76.0%; Score 38; DB 10; Length 513;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 120 GHSPLQKC 127

RESULT 11
Q9PFF7 PRELIMINARY; PRT; 82 AA.
ID AC Q9PFF7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein xF0702.
GN Xylella fastidiosa.
OS Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RA MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Bonaccorsi A.A., Camargo L.E.A., Carriago D.M., Carrier H.,
RA Colauto N.B., Colombo C., Colombo C., Costa F.F., Costa-Neto C.M.,

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RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003913; AAF83512.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 82 AA; 9067 MW; BCDE6C81A85EA7ED CRC64;

Query Match      74.0%; Score 37; DB 16; Length 82;
Best Local Similarity 75.0%; Pred. No. 6;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDKC 8
Db 59 GHSPLQKC 66

RESULT 12
Q09937 PRELIMINARY; PRT; 482 AA.
ID AC Q09937;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 53.8 kDa protein.
GN C53C9.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid C53C9.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28734; AAB52604.1; -
DR HSSP; Q54397; 1BL8.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003091; K_channel.

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DR InterPro: IPR003131; K_tetra.
DR InterPro: IPR000636; M_channel_nlg.
DR Pfam: PF00520; Ion_trans; 1.
DR Pfam: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Hypothetical protein.
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Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLDKC 8
DB 155 HRPLDVC 161

RESULT 13
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ID Q9SI49
AC Q9SI49;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative cytochrome P450.
GN AT2G14100.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
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RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X.; Kaul S.; Rounsley S.D.; Shea T.P.; Benito M.-I.; Town C.D.;
RA Fujii C.Y.; Mason T.M.; Boyman C.L.; Barnstead M.E.; Feldblum T.V.;
RA Buell C.R.; Ketchum K.A.; Lee J.J.; Ronning C.M.; Koo H.; Moffat K.S.;
RA Cronin L.A.; Shen M.; VanAken S.E.; Umayam L.; Tallon L.J.; Gill J.E.;
RA Adams M.D.; Carrara A.J.; Creasy T.H.; Goodman H.M.; Somerville C.R.;
RA Copenhaver G.P.; Preuss D.; Nierman W.C.; White O.; Eissen J.A.;
RA Salzberg S.L.; Fraser C.M.; Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana";
RL Nature 402:761-768(1999).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AC007197; AAD25850.1;
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR001783; Lum_binding.
DR Pfam: PF00667; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
DR PROSITE: PS00693; LUM_BINDING; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 518 AA; 58814 MW; 221B94886F602F84 CRC64;

Query Match 74.0%; Score 37; DB 10; Length 518;
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Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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DB 112 GHPPIDEC 119

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AC Q96989;
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DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CDC45L protein (LD35753P).
GN CDC45L OR CG3658.
OS Drosophila melanogaster (Fruit fly).
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OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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RN [1]
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RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D.; Celniker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.;
RA Amanatides P.G.; Scherer S.E.; Li P.W.; Hoskins R.A.; Galle R.F.;
RA George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N.;
RA Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.;
RA Brandon R.C.; Rogers J.-H.C.; Blazer R.G.; Champagne M.; Pfeiffer B.D.;
RA Wan K.H.; Doyle C.; Baxter E.G.; Helt G.; Nelson C.R.; Miklos G.L.G.;
RA Abrial J.F.; Agbayani A.; An H.-J.; Andrews-Pfannkoch C.; Baldwin D.;
RA Ballev R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.;
RA Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandari D.; Bolshakov S.;
RA Borkova D.; Botchan M.R.; Bouck J.; Brokstein P.; Brotter P.;
RA Burtis K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.;
RA Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.;
RA de Pablos B.; Delcher A.; Deng Z.; Mays A.D.; Dew I.; Dietz S.M.;
RA Dodson K.; Doup L.E.; Downes M.; Dugan-Rocha S.; Dunkov B.C.; Dunn P.;
RA Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferreira S.; Fleischmann W.;
RA Fouts R.C.; Gabrielian A.E.; Garg N.S.; Gelbart W.M.; Glasser K.;
RA Glodek A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.;
RA Harris N.L.; Harvey D.; Heiman T.J.; Hernandez J.R.; Houck J.;
RA Hostin D.; Houston K.A.; Howland T.J.; Wei M.-H.; Ibegwam C.;
RA Jalali M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.;
RA Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai Z.;
RA Lasko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.;
RA Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; McPherson D.;
RA Merkulov G.; Milshina N.V.; Mobarry C.; Morris J.; Moshrefi A.;
RA Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muzny D.M.; Nelson D.L.;
RA Nelson D.R.; Nelson K.A.; Nixon K.; Nusskern D.R.; Pacle J.M.;
RA Palazzolo M.; Pittman G.S.; Pan S.; Pollard J.; Puri V.; Reese M.G.;
RA Reinert K.; Remington K.; Saunders R.D.C.; Scheeler F.; Shen H.;
RA Shue B.C.; Siden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.;
RA Spier E.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.;
RA Svirskas R.; Tector C.; Turner E.; Venter E.; Wang A.H.; Wang X.;
RA Wang Z.-Y.; Wasserman D.A.; Weinstock G.M.; Weissbach J.;
RA Williams S.M.; Woodage T.; Worley K.C.; Wu D.; Yang S.; Yao Q.A.;
RA Ye J.; Yeh R.-F.; Zaveri J.S.; Zhan M.; Zhang Q.; Zheng L.;
RA Zheng X.H.; Zhong F.N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.;
RA Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
[2]
RN
RP SEQUENCE FROM N.A.
RA Papagiannakis G.; Spanos L.; Bolshakov V.; Siden-Kiamos I.; Louis C.;
RT "Sequencing the distal x chromosome of Drosophila melanogaster";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN
RP SEQUENCE FROM N.A.
RA Benos P.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[4]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=99160479; PubMed=10051334;
RA Shaikh T.H.; Gottlieb S.; Sellinger B.; Chen F.; Roe B.A.; Oakey R.J.;
RA Emanuel B.S.; Budarf M.L.;
RT "Characterization of CDC45L: a gene in the 22q11.2 deletion region
RT expressed during murine and human development.";
RL Mamm. Genome 10:322-326(1999).
[5]
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RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;

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RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Campe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Faregas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003419; AAF45579.1; +
DR EMBL; AL109630; CAB51681.1; -
DR EMBL; AF081540; AAD09003.1; -
DR EMBL; AY051861; AAX93285.1; -
DR FlyBase; FBgn0026143; CDC45L.
DR InterPro; IPR003874; CDC45-like.
DR Pfam; PF02724; CDC45; 1.
SQ SEQUENCE 575 AA; 65890 MW; A58341D46DEFE618 CRC64;

Query Match 74.0%; Score 37; DB 5; Length 575;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 101 HRPLDVC 107

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AC Q9VA50;
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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG9713 protein.
GN CG9713.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003774; AAF57073.1; -
DR FlyBase; FBgn0039793; CG9713.
DR InterPro; IPR005123; 2OG-feil_Oxy.
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DB 539 GHRPLEK 545

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Job time : 26.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-424-940A-2

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Sequence: 1 GHRPLDKC 8

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	41	82.0	25	9	US-10-142-935-4
3	41	82.0	30	9	US-10-131-343-5
4	41	82.0	30	9	US-10-131-346-5
5	41	82.0	30	9	US-10-131-546-5
6	41	82.0	491	9	US-10-017-724-6
7	36	72.0	10	9	US-10-142-935-9
8	36	72.0	15	9	US-10-142-935-8
9	36	72.0	20	9	US-10-142-935-5
10	35	70.0	1203	10	US-09-799-875-5
11	34	68.0	245	8	US-08-424-5508-38
12	34	68.0	370	10	US-09-925-300-1483
13	32	64.0	785	10	US-09-801-368-348
14	32	64.0	855	9	US-10-072-094-9
15	32	64.0	855	10	US-09-817-913-13
16	32	64.0	855	10	US-09-817-538-13
17	32	64.0	967	9	US-09-563-728A-30
18	32	64.0	967	10	US-09-817-913-7
19	32	64.0	967	10	US-09-817-538-7

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21	32	64.0	1084	9	US-10-173-539-12	Sequence 12, Appli
22	31	62.0	35	10	US-09-864-761-35105	Sequence 35105, A
23	31	62.0	43	10	US-09-864-761-46135	Sequence 46135, A
24	31	62.0	66	10	US-09-071-838-296	Sequence 296, App
25	31	62.0	111	9	US-09-764-891-5127	Sequence 5127, Ap
26	31	62.0	228	10	US-09-815-242-12032	Sequence 12032, A
27	31	62.0	384	10	US-09-825-414-34	Sequence 54, Appli
28	31	62.0	385	9	US-10-147-003-2	Sequence 2, Appli
29	31	62.0	1139	9	US-09-971-490-5	Sequence 5, Appli
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31	30	60.0	41	10	US-09-864-761-36299	Sequence 36299, A
32	30	60.0	68	9	US-10-102-806-465	Sequence 465, App
33	30	60.0	73	9	US-10-073-961-288	Sequence 288, App
34	30	60.0	73	10	US-09-764-887-288	Sequence 288, App
35	30	60.0	117	9	US-09-975-719-33	Sequence 33, Appli
36	30	60.0	170	9	US-09-975-719-158	Sequence 158, App
37	30	60.0	183	9	US-09-791-279-157	Sequence 157, App
38	30	60.0	206	9	US-09-791-279-129	Sequence 129, App
39	30	60.0	233	10	US-09-216-393-110	Sequence 110, App
40	30	60.0	294	9	US-09-738-626-4538	Sequence 4538, Ap
41	30	60.0	313	9	US-09-764-891-4243	Sequence 4243, Ap
42	30	60.0	359	9	US-10-060-036-179	Sequence 179, App
43	30	60.0	359	12	US-10-029-654-12	Sequence 12, Appli
44	30	60.0	363	10	US-09-815-242-11949	Sequence 11949, A
45	30	60.0	401	9	US-10-103-313-347	Sequence 347, App

ALIGNMENTS

RESULT 1
US-10-142-935-6
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; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAG
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 2002-05-13
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-6

Query Match 82.0%; Score 41; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 GHRPLDK 7
Db 10 GHRPLDK 16
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RESULT 2
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; Sequence 4, Application US/10142935
; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAG
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 2002-05-13
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072

; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
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; SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-4

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RESULT 3

US-10-131-543-5
; Sequence 5, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131.543
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-543-5

Query Match 82.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 4 GHRPLDK 10

RESULT 4

US-10-131-346-5
; Sequence 5, Application US/10131346
; Publication No. US2003010389A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131.346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-346-5

Query Match 82.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 4 GHRPLDK 10

RESULT 5

US-10-131-546-5
; Sequence 5, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyt, John E.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; TITLE OF INVENTION: CHROMANS
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131.546
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-546-5

Query Match 82.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 4 GHRPLDK 10

RESULT 6

US-10-017-724-6
; Sequence 6, Application US/10017724
; Publication No. US2003009958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6

; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo Sapiens

US-10-017-724-6

Query Match 82.0%; Score 41; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 45 GHRPLDK 51

RESULT 7

US-10-142-935-9
; Sequence 9, Application US/10142935
; Publication No. US2003004418A1

; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION

; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-10-142-935-9

Query Match 72.0%; Score 36; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 6
Db 5 GHRPLDK 10

RESULT 8

US-10-142-935-8
; Sequence 8, Application US/10142935
; Publication No. US2003004418A1

; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION

; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-10-142-935-8

Query Match 72.0%; Score 36; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 6

Db 10 GHRPLDK 15

RESULT 9

US-10-142-935-5
; Sequence 5, Application US/10142935
; Publication No. US2003004418A1

; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION

; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-10-142-935-5

Query Match 72.0%; Score 36; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 6
Db 15 GHRPLDK 20

RESULT 10

US-09-799-875-5
; Sequence 5, Application US/09799875
; Patent No. US20020034780A1

; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel

; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: No. US20020034780A1 Human Protein Kinases and Uses

; FILE REFERENCE: 35800/209996

; CURRENT APPLICATION NUMBER: US/09/799,875

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/182,059

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 09/659,287

; PRIOR FILING DATE: 2000-09-12

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1203

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-799-875-5

Query Match 70.0%; Score 35; DB 10; Length 1203;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 799 GHRPLSK 805

RESULT 11

US-08-424-550B-38
; Sequence 38, Application US/08424550B
; Patent No. US20020119447A1

; GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHÉRI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-38

Query Match 68.0%; Score 34; DB 8; Length 245;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GHRPLDKC 8
| ||| |
Db 25 GRPLAKC 32

RESULT 12
US-09-925-300-1483
; Sequence 1483, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1483
; LENGTH: 370

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1483

Query Match 68.0%; Score 34; DB 10; Length 370;
Best Local Similarity 71.4%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 HRPLDKC 8
| ||| |
Db 84 HMLDEC 90

RESULT 13
US-09-801-368-348
; Sequence 348, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fung
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 348
; LENGTH: 785
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-348

Query Match 64.0%; Score 32; DB 10; Length 785;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GHRPLDKC 8
| ||| |
Db 590 GEPLKCC 597

RESULT 14
US-10-072-094-9
; Sequence 9, Application US/10072094
; Publication No. US2003002538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTFARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-094-9

Query Match 64.0%; Score 32; DB 9; Length 855;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 437 GHRPLSR 443

RESULT 15
US-09-817-913-13
; Sequence 13, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfills, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-817-913-13

Query Match 64.0%; Score 32; DB 10; Length 855;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 437 GHRPLSR 443

Search completed: June 16, 2003, 16:16:37
Job time : 32.4667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:00:28 ; Search time 28 Seconds
(without alignments)
33.313 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41

Sequence: 1 GHRPLDK 7

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	7	8 AAP71314	Sequence of fibrin peptide antigenic
2	41	100.0	7	11 AAR05558	Beta-peptide used
3	41	100.0	7	15 AAR63269	Fibrin-specific ep
4	41	100.0	7	15 AAR63792	Human fibrin beta
5	41	100.0	8	9 AAP82686	Human fibrin beta
6	41	100.0	8	14 AAR44837	Synthetic beta-pep
7	41	100.0	8	15 AAR63270	Fibrin-specific ep
8	41	100.0	8	15 AAR65793	Residues 45-54 of
9	41	100.0	9	22 ABB76979	Fibrinogen A-alpha
10	41	100.0	10	16 AAW11931	

11	41	100.0	12	13	AAR28629	N-terminal human f
12	41	100.0	12	14	AAR44829	Human fibrin beta-
13	41	100.0	12	14	AAR44838	Human fibrin beta-
14	41	100.0	16	14	AAR44010	Scintigraph imagin
15	41	100.0	28	14	AAR40010	Human fibrin beta-
16	41	100.0	29	14	AAR42547	Leukocyte-binding
17	41	100.0	30	14	AAR42546	Leukocyte-binding
18	41	100.0	87	22	ABBI1339	Human beta-fibrino
19	41	100.0	118	21	AAG00151	Human secreted pro
20	41	100.0	140	22	AAU33273	Novel human secret
21	41	100.0	141	22	AAO10778	Human polypeptide
22	41	100.0	150	21	AAG00150	Human secreted pro
23	41	100.0	453	22	AAW78493	Human protein SEQ
24	41	100.0	491	16	AAR82243	Human protein SEQ
25	41	100.0	491	22	AAW78492	Human protein SEQ
26	41	100.0	495	22	AAW79475	Human protein SEQ
27	41	100.0	495	22	AAW79476	Human protein SEQ
28	41	100.0	495	22	AAW79477	Human protein SEQ
29	41	100.0	539	22	AAW78491	Human protein SEQ
30	37	90.2	923	22	ABBS9000	Drosophila melanog
31	36	87.8	11	21	AAI10666	Fibrinogen-beta pe
32	36	87.8	11	21	AAI10666	Fibrinogen-beta c
33	36	87.8	159	23	ABP30199	Streptococcus poly
34	36	87.8	165	23	ABP27176	Streptococcus poly
35	35	85.4	39	23	AAU91250	Mouse homologue of
36	35	85.4	41	22	ABG08987	Novel human diagno
37	35	85.4	202	22	AAW71790	Human olfactory re
38	35	85.4	305	22	AAW71593	Human olfactory re
39	35	85.4	305	22	AAW72216	Human olfactory re
40	35	85.4	305	22	AAW72243	Human olfactory re
41	35	85.4	305	22	AAW72250	Human olfactory re
42	35	85.4	305	22	AAW72356	Human OR-like poly
43	35	85.4	305	23	ABP51611	Human G protein co
44	35	85.4	505	22	AAW95070	Human protein sequ
45	35	85.4	613	22	ABG08445	Novel human diagno

ALIGNMENTS

RESULT 1

ID	Sequence	Location/Qualifiers
AAW71314	AAW71314 standard; peptide; 7 AA.	
XX	AAW71314;	
AC		
XX		
DT	03-OCT-2002 (updated)	
DT	19-JUN-1991 (first entry)	
XX		
DE	Sequence of fibrin immunogen for the prepn. of monoclonal antibodies (Mabs).	
DE		
XX		
KW	Fibrin-specific monoclonal antibody; screening.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference	/label= Lys-OH
FT		
XX		
FN	WO8706263-A.	
XX		
PD	22-OCT-1987.	
XX		
PF	14-APR-1987;	87WO-US00862.
XX		
PR	14-APR-1986;	86US-0851514.
XX		
PA	(GENO-) GEN HOSPITAL CORP.	
PA	(GENO-) GEN HOSPITAL CORP.	
PI	Matsueda GR, Haber E;	
XX		

DR WPI; 1987-306855/43.
 XX Screening of fibrin-specific monoclonal antibodies - by contact
 PT with immobilised crosslinked fibrin clot and screening with
 PT detectable labelling step
 XX
 XX Disclosure; Page 7; 41pp; English.
 XX
 CC The MABs are specific to fibrin without fibrinogen cross-reactivity.
 CC They have increased binding to in vitro and in vivo thrombi. The
 CC MABs can be used in immunoassays for fibrin in the presence of
 CC fibrinogen or other proteins. They can be used as immunoaffinity
 CC ligands for the purification of fibrin.
 CC (Updated on 03-OCT-2002 to add missing OS field.)
 XX
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7
 RESULT 2
 AAR05558
 ID AAR05558 standard; peptide: 7 AA.
 XX
 AC AAR05558;
 XX
 DT 11-OCT-1990 (first entry)
 DE
 XX Peptide antigenic to fibrin.
 KW fibrin; fibrinogen; thrombi; immunoaffinity.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /label-His or Pro
 FT Misc-difference 4 /label-Pro or Val
 FT Misc-difference 5 /label-Leu or Val
 FT Misc-difference 6 /label-Asp or Glu
 FT Misc-difference 7 /label-Lys or Arg
 XX
 PN US4927916-A.
 XX
 PD 22-MAY-1990.
 XX
 PF 30-JAN-1986; 8605-0824228.
 XX
 PR 23-APR-1984; 8405-0603155.
 PR 30-JAN-1986; 8605-0824228.
 XX
 XX (GEHO-) GEN HOSPITAL CORP.
 XX
 XX Matsueda GR, Haber E, Hui K;
 PI WPI; 1990-185723/24.
 DR
 XX Fibrin-specific monoclonal antibodies -
 PT lacking fibrinogen cross-reactivity, obtd. using peptide(s)
 PT comprising fibrin-specific epitopic sequences.
 XX
 XX Claim 1; Page 17; 12pp; English.
 PS
 XX

CC Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be
 CC raised without cross-reactivity to fibrinogen. They are
 CC particularly useful in detection of fibrin and thrombi.
 XX
 XX SQ Sequence 7 AA;
 Query Match 100.0%; Score 41; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7
 RESULT 3
 AAR63269
 ID AAR63269 standard; peptide: 7 AA.
 XX
 AC AAR63269;
 XX
 DT 21-JUL-1995 (first entry)
 DE
 XX Beta-peptide used to raise monoclonal antibody 59D8.
 XX
 KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
 KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
 KW coronary stent implantation; adjunctive therapy; fibrinogen;
 KW haemorrhage.
 XX
 OS Synthetic.
 XX
 PN WO9425491-A.
 XX
 PD 10-NOV-1994.
 XX
 PF 03-MAY-1994; 94WO-US04881.
 XX
 PR 03-MAY-1993; 93US-00586699.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (UYEM-) UNIV EMORY.
 XX
 PI Bode C, Haber E, Runge M;
 XX
 XX WPI; 1994-358195/44.
 DR
 XX Fibrin-binding antibody linked to thrombin inhibitor - useful for
 XX preventing blood coagulation by specifically targeting inhibitor
 XX to site of thrombin activity
 XX
 XX Example 1; Page 13; 53pp; English.
 PS
 XX This sequence represents beta-peptide which was used to raise the
 XX monoclonal antibody 59D8. The antibody binds fibrin and may be used
 XX in the chimeric molecule of the invention. The chimeric molecule
 XX further comprises a thrombin inhibitor linked to the fibrin-binding
 XX antibody through a covalent linkage. The chimeric molecule allows
 XX fibrin-specific antibody targeting of hirudin and other thrombin
 XX inhibitors, which is more potent than thrombin on its own. The epitope
 XX to which 59D8 binds becomes available only after thrombin cleaves
 XX fibrinopeptide B. The chimeric protein may be used for preventing
 XX coagulation of the blood. Anti-thrombin targeting can be esp. useful
 XX in highly thrombogenic situations such as coronary stent implantation
 XX and can be used as an adjunctive therapy with highly selective
 XX thrombolytic agents. The thrombin inhibitor is localised to sites
 XX of thrombin activity by the antibody which binds to thrombin but does
 XX not cross react with uncleaved fibrinogen. The selectivity of
 XX inhibition allows the total amount of thrombin inhibitor used to be
 XX substantially reduced, resulting in a reduced potential for generalised
 XX haemorrhaging.
 XX
 XX SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7

RESULT 4
 AAR65792
 ID AAR65792 standard; peptide; 7 AA.
 AC AAR65792;
 DT 26-JUN-1995 (first entry)
 DE Fibrin-specific epitopic peptide.
 KW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
 KW antifibrin-specific monoclonal antibodies.
 OS Synthetic.
 PN US5357042-A.
 XX 18-OCT-1994.
 XX 23-APR-1984; 84US-0603155.
 XX 23-APR-1984; 84US-0603155.
 PR 30-JAN-1986; 86US-0824228.
 PR 22-DEC-1989; 89US-0454954.
 PR 24-AUG-1992; 92US-0932729.
 XX (GEHO) GEN HOSPITAL CORP.
 XX Haber E, Hui K, Matsueda GR;
 PI WPI; 1994-332411/41.
 XX Synthetic epitopic peptide(s) of variable length - capable of
 PT eliciting fibrin specific antibodies free of fibrinogen
 PT cross-reactivity.
 XX Claim 2; Column 18; 12pp; English.
 PS AAR65789-R65794 are synthetic peptides comprising fibrin-specific
 CC epitopic sequences, they can be used to prepare hybridoma cell
 CC lines, which produce antifibrin-specific monoclonal antibodies
 CC substantially devoid of fibrinogen cross-reactivity. These
 CC antibodies are useful in the in vivo and in vitro detection
 CC of thrombi and fibrin deposits.
 XX Sequence 7 AA;
 SO Query Match 100.0%; Score 41; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7

RESULT 5
 AAP82686
 ID AAP82686 standard; peptide; 8 AA.
 XX AAP82686;
 AC AAP82686;
 DT 05-DEC-1990 (first entry)

XX Human fibrin beta chain N-terminal.
 DE Fibrin; beta chain; N-terminal; monoclonal antibody; thrombosis.
 KW Synthetic.
 OS JP63093800-A.
 PN 25-APR-1988.
 XX 08-OCT-1986; 86JP-0237876.
 PF 08-OCT-1986; 86JP-0237876.
 PR (MITN) MITSUBISHI GAS CHEM KK.
 XX WPI; 1988-152086/22.
 DR New anti-human fibrin monoclonal antibody for diagnosing thrombosis
 XX - prepd. from hybridoma obt'd. by applying cell fusion mouse spleen
 PT and mouse myeloma cells, and measures human fibrin.
 CC Claim 1; Page 1; 8pp; Japanese.
 XX The peptide is linked to a carrier protein via a linking agent and
 CC used to immunise mice. The mouse spleen cells and amyeloma cell
 CC line can be fused to produce a hybridoma secreting MAb's which bind
 CC specifically to human fibrin but not fibrinogen.
 XX Sequence 8 AA;
 SO Query Match 100.0%; Score 41; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 DB 1 GHRPLDK 7

RESULT 6
 AAR44837
 ID AAR44837 standard; peptide; 8 AA.
 XX AAR44837;
 AC AAR44837;
 DT 20-JUN-1994 (first entry)
 XX Human fibrin beta-chain N-terminal peptide A.
 DE Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 XX Synthetic.
 OS JP05304992-A.
 PN 19-NOV-1993.
 PD 17-JUN-1992; 92JP-0158301.
 PF 20-JUN-1991; 91JP-0148936.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX WPI; 1993-408334/51.
 DR Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX

PS Example 1; Page 14; 38pp; Japanese.

XX Human fibrin beta-chain peptides A and B were synthesised and coupled
CC to BSA for injection into mice. The peptides were used to raise
CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
CC are used in the production of bispecific monoclonal antibodies
CC which also recognise truncated tPA muteins lacking the finger, EGF and
CC Kringle 1 domains.

XX Sequence 8 AA;

Query Match 100.0%; Score 41; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 7

AAR63270
ID AAR63270 standard; peptide; 8 AA.

XX AC AAR63270;

XX DT 21-JUL-1995 (first entry)

XX DE Synthetic beta-peptide used to raise monoclonal antibody 59D8.

XX KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;

XX KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;

XX KW coronary stent implantation; adjunctive therapy; fibrinogen;

XX KW haemorrhage.

XX OS Synthetic.

XX PN WO9425491-A.

XX PD 10-NOV-1994.

XX PF 03-MAY-1994; 94WO-US04881.

XX PR 03-MAY-1993; 93US-0058699.

XX PA (HARD) HARVARD COLLEGE.

XX PA (UYEM-) UNIV EMORY.

XX PI Bode C, Haber E, Runge M;

XX DR WPI; 1994-358195/44.

XX Fibrin-binding antibody linked to thrombin inhibitor - useful for
PT preventing blood coagulation by specifically targeting inhibitor
PT to site of thrombin activity

PS Example 1; Page 14; 53pp; English.

XX This sequence represents a synthetic beta-peptide which was used to
CC immunopurify the monoclonal antibody 59D8 which was raised against
CC beta-peptide (see also AAR63269). The antibody binds fibrin and may be
CC used in the chimeric molecule of the invention. The chimeric molecule
CC further comprises a thrombin inhibitor linked to the fibrin-binding
CC antibody through a covalent linkage. The chimeric molecule allows
CC fibrin-specific antibody targeting of hirudin and other thrombin
CC inhibitors, which is more potent than thrombin on its own. The epitope
CC to which 59D8 binds becomes available only after thrombin cleaves
CC fibrinopeptide B. The chimeric protein may be used for preventing
CC coagulation of the blood. Anti-thrombin targeting can be esp. useful
CC in highly thrombogenic situations such as coronary stent implantation
CC and can be used as an adjunctive therapy with highly selective
CC thrombolytic agents. The thrombin inhibitor is localised to sites
CC of thrombin activity by the antibody which binds to thrombin but does

CC not cross react with uncleaved fibrinogen. The selectivity of
CC inhibition allows the total amount of thrombin inhibitor used to be
CC substantially reduced, resulting in a reduced potential for generalised
CC haemorrhaging.

XX Sequence 8 AA;

Query Match 100.0%; Score 41; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 8

AAR65793
ID AAR65793 standard; peptide; 8 AA.

XX AC AAR65793;

XX DT 26-JUN-1995 (first entry)

XX DE Fibrin-specific epitopic peptide.

XX KW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
XX KW antifibrin-specific monoclonal antibodies.

XX OS Synthetic.

XX PH Key Location/Qualifiers

XX FT Misc-difference 8 /note= "May be absent and if present
XX FT may be bonded to keyhole limpet
XX FT hemocyanin."

XX PN US5357042-A.

XX PD 18-OCT-1994.

XX PF 23-APR-1984; 84US-0603155.

XX PR 23-APR-1984; 84US-0603155.

XX PR 30-JAN-1986; 86US-0824228.

XX PR 22-DEC-1989; 89US-0454954.

XX PR 24-AUG-1992; 92US-0932729.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PI Haber E, Hui K, Matsueda GR;

XX DR WPI; 1994-332411/41.

XX Synthetic epitopic peptide(s) of variable length - capable of
PT eliciting fibrin specific antibodies free of fibrinogen
PT cross-reactivity.

XX Claim 3; Column 18; 12pp; English.

XX AAR65789-R65794 are synthetic peptides comprising fibrin-specific
CC epitopic sequences, they can be used to prepare hybridoma cell
CC lines, which produce antifibrin-specific monoclonal antibodies
CC substantially devoid of fibrinogen cross-reactivity. These
CC antibodies are useful in the in vivo and in vitro detection
CC of thrombi and fibrin deposits.

XX Sequence 8 AA;

Query Match 100.0%; Score 41; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7
  |||||
  1 GHRPLDK 7

RESULT 9
ABB76979
ID ABB76979 standard; peptide; 9 AA.
XX AC
XX ABB76979;
XX
XX
XX 22-JUL-2002 (first entry)
XX
XX Residues 45-54 of human fibrinogen beta chain precursor.
XX
XX Anti-arthritis; anti-inflammatory; fibrin; rheumatoid polyarthritis;
XX KW human; fibrinogen beta chain.
XX
XX Homo sapiens.
XX OS
XX FR2795735-A1.
XX PN
XX 05-JAN-2001.
XX PD
XX 01-JUL-1999; 99FR-0008470.
XX PF
XX 01-JUL-1999; 99FR-0008470.
XX PR
XX
XX (UYTO-) UNIV TOULOUSE SABATIER PAUL.
XX PA
XX Serre G, Sebbag M;
XX PI
XX WPI; 2001-114394/13.
XX DR
XX
XX New citrulline-containing polypeptide from fibrin, useful for diagnosis
XX PT and treatment of rheumatoid polyarthritis
XX
XX Example 1; Page 12; 23pp; French.
XX PS
XX
XX The present invention relates to a citrulline (Cit) containing
XX CC polypeptide derived from all or part of the alpha- or beta-chains of
XX CC fibrin by substitution of at least one arginine residue by Cit. The Cit
XX CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
XX CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
XX CC therapeutically for neutralising the RP-associated autoimmune response.
XX CC The present sequence is a fragment (residues 45-54) of the human
XX CC fibrinogen beta chain precursor, which was used in an example from the
XX CC invention.
XX
XX Sequence 9 AA:
XX SQ
  Query Match 100.0%; Score 41; DB 22; Length 9;
  Best Local Similarity 100.0%; Pred. No. 7.8e+05;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7
  |||||
  1 GHRPLDK 7

RESULT 10
AAW11931
ID AAW11931 standard; peptide; 10 AA.
XX AC
XX AAW11931;
XX
XX
XX 02-APR-1997 (first entry)
XX DT
XX Fibrinogen A-alpha-chain residues 17-26.
XX DE
XX Monoclonal; antibody; human; soluble; fibrin; fibrinogen;
XX KW urea-treated; des-AAB; A-alpha-chain; immunoassay; diagnosis;
XX KW disseminated intravascular coagulation.

```

DR WPI; 1992-383677/47.
 XX BI-specific antibody useful for treating thrombotic obstructive
 PT diseases e.g. cardiac infarction - comprises antithrombus
 PT antibody variable region and anti-thrombolytic substance antibody
 PT 3 variable region with no heavy chain constant region domains 2 and
 XX
 XX Disclosure; Page 3; 30pp; English.
 XX
 CC This sequence represents an N-terminal peptide of human fibrin. It
 CC was used in the production of bispecific monoclonal antibodies which
 CC are specific for fibrins, but do not bind fibrinogen, and are
 CC specific for anti-thrombolytic substance. The compsn. contg. these
 CC Abs lacks the side effects of prior art Ab targeted thrombolytic
 CC agents and has enhanced thrombolytic activity.
 XX
 XX Sequence 12 AA;
 SQ
 Query Match 100.0%; Score 41; DB 13; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 1 GHRPLDK 7
 RESULT 12
 AAR44829
 ID AAR44829 standard; peptide; 12 AA.
 XX
 AC AAR44829;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Human fibrin beta-chain N-terminal peptide (1-11)-Cys.
 XX
 KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..11
 FT /note= "human fibrin beta-chain residues 1-11"
 FT Modified-site 12
 FT /note= "BSA carrier is attached to Cys"
 XX
 PN JP05304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-408334/51.
 XX
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX
 PS Disclosure; Page 9; 30pp; Japanese.
 XX
 CC Human fibrin beta-chain N-terminal peptide (1-11)-Cys was
 CC synthesised and coupled to BSA for injection into mice. The peptide
 CC was used to raise antibodies to human fibrin. Monoclonal antibodies
 CC specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins

CC lacking the finger, EGF and Kringle 1 domains.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 41; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 1 GHRPLDK 7
 RESULT 13
 AAR44838
 ID AAR44838 standard; peptide; 12 AA.
 XX
 AC AAR44838;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Human fibrin beta-chain peptide B.
 XX
 KW Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 XX
 OS Synthetic.
 XX
 PN JP05304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-408334/51.
 XX
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX
 PS Example 1; Page 14; 38pp; Japanese.
 XX
 CC Human fibrin beta-chain peptides A and B were synthesised and coupled
 CC to BSA for injection into mice. The peptides were used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
 CC are used in the production of bispecific monoclonal antibodies
 CC which also recognise truncated tPA muteins lacking the finger, EGF and
 CC Kringle 1 domains.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 41; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB |||||
 6 GHRPLDK 12
 RESULT 14
 AAR44830
 ID AAR44830 standard; peptide; 16 AA.
 XX
 AC AAR44830;
 XX
 DT 20-JUN-1994 (first entry)
 XX

DE Human fibrin beta-chain internal peptide fragment.
XX
KW Tissue plasminogen activator; t-PA; mutelns; fibrin; antigen;
KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
KW antithrombotic agent; bispecific antibody.
OS Synthetic.
XX
XX JP05304992-A.
XX
XX 19-NOV-1993.
XX
XX 17-JUN-1992; 92JP-0158301.
XX
XX 20-JUN-1991; 91JP-0148936.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX WPI; 1993-408334/51.
XX
XX Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
PT having increased thrombolytic activity and specificity and
PT reduced reactivity to fibrinogen
XX
XX Disclosure; Page 9; 38pp; Japanese.
XX
XX Human fibrin internal peptide fragment was identified as a
CC candidate immunogen to raise antibodies to human fibrin. Monoclonal
CC antibodies specific for fibrin are used in the production of bispecific
CC monoclonal antibodies which also recognise truncated tPA mutelns
CC lacking the finger, EGF and Kringle 1 domains.
XX
XX
SQ Sequence 16 AA;
Query Match 100.0%; Score 41; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
Db 6 GHRPLDK 12
RESULT 15
AAR40010
ID AAR40010 standard; peptide; 28 AA.
XX
XX AAR40010;
XX
XX 23-MAY-1994 (first entry)
XX
XX Scintigraph imaging agent specific binding peptide.
XX
XX Reagent; site imaging; technetium-99M labelled; peptide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 28
XX /note- "C-terminal amide"
XX
XX WO9321962-A.
XX
XX 11-NOV-1993.
XX
XX 19-APR-1993; 93WO-US03687.
XX
XX 30-APR-1992; 92US-0871282.
XX
XX (DIAT-) DIATECH INC.
XX
XX Buttram S, Civitello ER, Dean RT, Lister-James J, McBride W;
XX

DR WPI; 1993-368429/46.
XX
XX Reagents for preparing scintigraphic imaging agents - contg.
PT technetium-99M labelled peptide(s) contg. 3-100 aminoacid(s)
XX
XX Claim 35; Page 39; 55pp; English.
XX
XX The sequence is that of a specific binding peptide used as part of
CC a reagent for preparing a scintigraphic imaging agent for imaging
CC sites within a mammalian body. In this the peptide is covalently
CC linked to a radiolabel-binding moiety which is capable of forming
CC a complex with a radioisotope, pref. technetium-99M.
XX
XX
SQ Sequence 28 AA;
Query Match 100.0%; Score 41; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7
Db 1 GHRPLDK 7
Search completed: June 16, 2003, 16:03:14
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:01:49 ; Search time 11.6667 Seconds
(without alignments)
57.681 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41

Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	41	100.0	31	2 A05297	fibrinogen beta ch
2	41	100.0	491	1 FGHUB	fibrinogen beta ch
3	36	87.8	201	2 C95399	probable transcrip
4	36	87.8	468	1 FGBOR	fibrinogen beta ch
5	36	87.8	1490	2 T47840	multi resistance p
6	35	85.4	463	2 A38463	fibrinogen beta ch
7	34	82.9	673	2 T40817	zinc finger protei
8	34	82.9	795	2 A84608	hypothetical prote
9	33	80.5	225	2 A75550	MutT/nudix family
10	33	80.5	1058	2 D82654	ankyrin-like prote
11	32	78.0	423	2 T20233	hypothetical prote
12	32	78.0	476	2 E87040	acyl-CoA synthase
13	32	78.0	485	2 F70464	hypothetical prote
14	32	78.0	611	2 D84423	probable WD-40-rep
15	32	78.0	878	2 T17245	hypothetical prote
16	31	75.6	42	2 B92087	myelin basic prote
17	31	75.6	169	1 MBOR	myelin basic prote
18	31	75.6	169	2 F72465	hypothetical prote
19	31	75.6	176	2 D86434	hypothetical prote
20	31	75.6	215	2 S23432	pyroglutamyl-pepti
21	31	75.6	225	2 T25957	hypothetical prote
22	31	75.6	228	2 D83071	probable ATP-bindi
23	31	75.6	250	2 T46417	hypothetical prote
24	31	75.6	309	2 T19389	hypothetical prote
25	31	75.6	343	2 E71149	hypothetical prote
26	31	75.6	344	2 H87710	hypothetical prote
27	31	75.6	345	2 D96011	probable oxidoredu
28	31	75.6	374	2 S77072	queuine tRNA-ribos
29	31	75.6	424	2 C69077	thiamin biosynthes

30	31	75.6	473	2 G70607	probable fadB36 pr
31	31	75.6	480	2 A71093	proline-tRNA liqas
32	31	75.6	480	2 G75072	prolyl-tRNA synthe
33	31	75.6	548	2 C75499	cytidine/deoxycyti
34	31	75.6	633	2 E31265	ipaa protein - Shi
35	31	75.6	648	2 C83023	probable oxidoredu
36	31	75.6	1970	2 T03284	myoblast city prot
37	31	75.6	3670	2 T36249	CDA peptide synthe
38	30	73.2	50	1 INTO2	insulin 2 - loadfi
39	30	73.2	104	2 H83530	hypothetical prote
40	30	73.2	123	2 T15030	hypothetical prote
41	30	73.2	127	2 G95291	hypothetical prote
42	30	73.2	162	2 E87094	probable phosphope
43	30	73.2	184	2 A37041	homeotic protein A
44	30	73.2	202	2 AE3377	queuine tRNA-ribos
45	30	73.2	213	2 T35433	hypothetical prote

ALIGNMENTS

RESULT 1

A05297
fibrinogen beta chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996
C:Accession: B94308; A03123; A37512; A05297; B37512; D03118
R:Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A:Title: Studies of the structure of canine fibrinogen.
A:Reference number: A94308; MUID:76081726; PMID:1198547
A:Accession: B94308
A:Molecule type: protein
A:Residues: 1-31 <BIR>
R:Blomback, B.; Blomback, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A:Title: Studies on fibrinopeptides from mammals.
A:Reference number: A03118
A:Accession: A03123
A:Molecule type: protein
A:Residues: 1-19 <BLO>
R:Krajewski, T.; Blomback, B.
Acta Chem. Scand. 22, 1339-1346, 1968
A:Reference number: A37512; MUID:69066367; PMID:5727635
A:Accession: A37512
A:Molecule type: protein
A:Residues: 1-19 <KRA>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen di
C:Keywords: blood coagulation; liver; plasma; sulfoprotein
F:1-19/Product: fibrinopeptide B #status experimental <APT>
F:2/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
F:3/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 100.0%; Score 41; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.054; Mismatches 0; Indels 0; Gaps 0;
Matches ; ; Conservative ; ;

Oy 1 GHRPLDK 7
|||||
Db 20 GHRPLDK 26

RESULT 2

FGHUB
fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000
C:Accession: B43568; A90469; I37389; A94433; A90437; A94309; G54223; A03121
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.

A:Reference number: A90041; MUID:84305751; PMID:6383194
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A:Title: Cloning of fibrinogen genes and their cDNA.
A:Reference number: A90038; MUID:83254384; PMID:6575700
A:Contents: annotation
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the alpha COC
A:Reference number: A37117; MUID:90337977; PMID:2143188
A:Contents: annotation; hementin cleavage site
A:Note: hementin, a protease from Haementeria ghilianii, the giant South American le
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cl
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-sta
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Genetics:
A:Gene: GDB:FCB
A:Cross-references: GDB:119130; OMIM:134830
A:Map position: 4q28-4q28
A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PI
ins are contained in the core. Two three-chain coiled coils emerge from this core an
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized i
A:Pathway: blood coagulation
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen dis
C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutam
F:1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
F:31-491/Product: fibrinogen beta chain #status experimental <MAT>
F:31-44/Product: fibrinopeptide B #status experimental <APT>
F:45-491/Product: fibrin beta chain #status experimental <PGB>
F:45-47/Region: polymerization site
F:99-228/Domain: fibrinogen disulfide ring homology <FDR>
F:238-487/Domain: fibrinogen beta/gamma homology <FBG>
F:31/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status.exp
F:44-45/Cleavage site: Arg-gly (thrombin) #status.experimental
F:95/Disulfide bonds: interchain (to alpha-55) #status.experimental
F:106/Disulfide bonds: interchain (to alpha-68) #status.experimental
F:110/Disulfide bonds: interchain (to gamma-45) #status.experimental
F:223/Disulfide bonds: interchain (to alpha-184) #status.experimental
F:227/Disulfide bonds: interchain (to gamma-161) #status.experimental
F:231-316,241-270,424-437/Disulfide bonds: #status.experimental
F:394/Binding site: carbohydrate (Asn) (covalent) #status.experimental

Query Match 100.0%; Score 41; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||||
Db 45 GHRPLDK 51

RESULT 3
C95399
probable transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) m
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: C95399
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.;
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh,
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium mel
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: C95399
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <GB>
A:Cross-references: GDB:AE065757.1; PTD:gl4524255; GSPDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galbert, F.; Finan, R.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R.;
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma2008
 A:Genome: plasmid

Query Match 87.8%; Score 36; DB 2; Length 201;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 |||||
 DB 175 GHRPLD 180

RESULT 4

FCBOB

fibrinogen beta chain - bovine
 N:Contains: fibrinopeptide B
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996
 C:Accession: A03122; B03117; B37507; A37513; S02443
 R:Blomback, B.; Doolittle, R.F.
 Acta Chem. Scand. 17, 1816-1819, 1963
 A:Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
 A:Reference number: A03122
 A:Accession: A03122
 A:Molecule type: protein
 A:Residues: 1-4 <BL0>
 R:Sjoquist, J.; Blomback, B.; Wallen, P.
 Ark. Kemi 16, 425-436, 1960
 A:Title: Amino acid sequence of bovine fibrinopeptides.
 A:Reference number: A03117
 A:Accession: B03117
 A:Molecule type: protein
 A:Residues: 5-21 <SJO>
 R:Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
 A:Reference number: A37507; MUID:79164394; PMID:434821
 A:Accession: B37507
 A:Molecule type: protein
 A:Residues: 22-53 <MAR>
 R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
 A:Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
 A:Reference number: A37513; MUID:81199473; PMID:6262803
 A:Accession: A37513
 A:Molecule type: mRNA
 A:Residues: 44-468 <CHU>
 R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
 FEBS Lett. 232, 56-60, 1988
 A:Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
 A:Reference number: S02443; MUID:88211875; PMID:2966748
 A:Accession: S02443
 A:Molecule type: protein
 A:Residues: 373-374 <MED>
 C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
 C:Superfamily: fibrinogen is a hexamer containing two sets of three nonidentical chains (alf
 F:76-205/Domain: fibrinogen disulfide ring homology <FDR>
 F:215-464/Domain: fibrinogen beta/gamma homology <FBG>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:6/Binding site: sulfate (Tyr) (covalent) #status experimental

F:21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
 F:371/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:372-373/Cleavage site: Arg-Thr (Plasmin) #status experimental
 Query Match 87.8%; Score 36; DB 1; Length 468;
 Best Local Similarity 85.7%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 |||||
 DB 22 GHRPYDK 28

RESULT 5

T47840

multi resistance protein homolog - Arabidopsis thaliana
 N:Alternate names: protein T209.140
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
 C:Accession: T47840
 R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner,
 submitted to the Protein Sequence Database, February 2000
 A:Reference number: Z24475
 A:Accession: T47840
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1490 <NYA>
 A:Cross-references: EMBL:AL138658
 A:Experimental source: cultivar Columbia; BAC clone T209
 C:Genetics:
 A:Map position: 3
 A:introns: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3; 1369/1; 1449/
 A:Note: T209.140
 C:Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homo

Query Match 87.8%; Score 36; DB 2; Length 1490;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 |||||
 DB 1226 GHRPLD 1231

RESULT 6

A38463

fibrinogen beta chain - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
 C:Accession: A38463
 R:Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
 Biochemistry 30, 3290-3294, 1991
 A:Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavag
 A:Reference number: A38463; MUID:91182745; PMID:2009266
 A:Accession: A38463
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-463 <WEI>
 A:Cross-references: GB:M58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen di
 F:73-202/Domain: fibrinogen disulfide ring homology <FDR>
 F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 85.4%; Score 35; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
 |||||
 DB 19 HRPLDK 24

RESULT 7

T40817
zinc finger protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
C:Accession: T40817
R:Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998
A:Reference number: 221949
A:Accession: T40817
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-673 <BC>
A:Cross-references: EMBL:AL032684; PIDN:CAA21808.1; GSPDB:GN00067; SPDB:SPBP8B7.23
A:Experimental source: strain 972h-; clone pl p8B7
C:Genetics:
A:Gene: SPDB:SPBP8B7.23
A:Map position: 2
A:Superfamily: RING finger homology
F:210-278/Domain: RING finger homology <RRN>

Query Match 82.9%; Score 34; DB 2; Length 673;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 160 GHRPMDK 166
|||||
-
RESULT 8
A84608
hypothetical protein At2g22020 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: A84608
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-795 <STO>
A:Cross-references: GB:AE002093; MID:94417294; PIDN:AD20419.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g22020
A:Map position: 2

Query Match 82.9%; Score 34; DB 2; Length 795;
Best Local Similarity 71.4%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 41 GHRPLER 47
|||||
-
RESULT 9
A75550
Mutr/nudix family protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: A75550
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75550
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-225 <WHI>
A:Cross-references: GB:AE001881; NID:96457853; PIDN:AAF09779.1; PID:964
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0192
A:Map position: 1

Query Match 80.5%; Score 33; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 178 GHRELDK 184
|||||
-
RESULT 10
D82654
ankyrin-like protein XF1640 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82654
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Se
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below.
A:Accession: D82654
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1058 <SIM>
A:Cross-references: GB:AE003991; GB:AE003849; NID:9106696; PIDN:AAF84449.1; GSPDB:G
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; F
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; L
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martin
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sav
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Sil
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjowski-Almeida, S.; Vettore, A.L
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1640

Query Match 80.5%; Score 33; DB 2; Length 1058;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
DB 497 GHRPVD 502
|||||
-
RESULT 11
T20233
hypothetical protein C54G4.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T20233
R:Wilkinson, J.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19241
A:Accession: T20233
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-423 <WIL>

A:Cross-references: EMBL:275533; PIDN:CAA99815.1; GSPDB:GN00019; CESP:C54G4.2
 A:Experimental source: clone C54G4

C:Genetics:
 A:Gene: CESP:C54G4.2

A:Map position: 1

A:Introns: 76/3; 172/3; 272/2; 312/1; 367/3

C:Superfamily: Caenorhabditis elegans hypothetical protein C54G4.2

Query Match 78.0%; Score 32; DB 2; Length 423;

Best Local Similarity 83.3%; Pred. No. 72;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPDLK 7

|||||

197 HRPDLR 202

RESULT 12

E87040 acyl-CoA synthase [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 15-Jun-2001

C:Accession: E87040

R.; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: E87040

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-476 <STO>

A:Cross-references: GB:AL450380; NID:g13093059; PIDN:CAC31432.1; GSPDB:GN00147

C:Genetics:

A:Gene: xclC

C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

Query Match 78.0%; Score 32; DB 2; Length 476;

Best Local Similarity 57.1%; Pred. No. 82;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

|||||

271 GHRPIER 277

RESULT 13

F70464

hypothetical protein aq_1912 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999

C:Accession: F70464

R.; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: F70464

A>Status: preliminary; nucleic acid sequence not shown; translation not shown.

A:Molecule type: DNA

A:Residues: 1-485 <AQF>

A:Cross-references: GB:AE000763; NID:g2984178; PIDN:AAC07717.1; PID:g2984185; GB:AE00065

A:Experimental source: strain VF5

C:Genetics:

A:Gene: aq_1912

Query Match 78.0%; Score 32; DB 2; Length 485;

Best Local Similarity 85.7%; Pred. No. 83;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

|||||

403 GHRPLSR 409

Search completed: June 16, 2003, 16:05:01

Job time : 13.6667 secs

Db 18 GDRPLDK 24

RESULT 14

D84423

Probable WD-40-repeat protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: D84423

R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

M.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.

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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:00:53 ; Search time 6.06667 Seconds
(without alignments)
47.857 Million cell updates/sec

Title: US-09-424-940A-1
Perfect score: 41
Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	41	100.0	31	FIBB_CANFA	P02677 canis famill
2	41	100.0	491	FIBB_HUMAN	P02675 homo sapien
3	36	87.8	468	FIBB_BOVIN	P02676 bos taurus
4	35	85.4	463	FIBB_CHICK	Q02020 gallus gall
5	35	85.4	479	FIBB_RAT	P14480 rattus norv
6	32	78.0	560	EF5_MOUSE	Q64355 mus musculu
7	32	78.0	1084	HDA4_CHICK	P83038 gallus gall
8	32	78.0	1084	HDA4_HUMAN	P56524 homo sapien
9	31	75.6	168	MBP_RABIT	P25274 oryctolagus
10	31	75.6	169	MBP_BOVIN	P02687 bos taurus
11	31	75.6	215	PCP_BACSU	P28618 bacillus su
12	31	75.6	333	MRWA_ZYMMO	Q9reg9 zymomonas m
13	31	75.6	363	TRMA_PSEFL	Q9rhs9 pseudomonas
14	31	75.6	374	TGT_SYNY3	Q55983 synchocyst
15	31	75.6	424	THC2_METHH	Q27617 methanobact
16	31	75.6	633	IPAA_SHIFL	P18010 shigella fi
17	30	73.2	50	INS2_RATSP	P01338 batrachoidi
18	30	73.2	184	HXB1_AMBME	P31357 ambystoma m
19	30	73.2	231	YEDJ_ECOLI	P46144 escherichia
20	30	73.2	253	ISPD_RALSO	Q8xwv3 ralstonia s
21	30	73.2	269	IOD3_RANCA	P49898 rana catesb
22	30	73.2	285	TRUA_PSEAE	O87016 pseudomonas
23	30	73.2	334	ACOD_PIG	O02858 sus scrofa
24	30	73.2	344	CD2_MOUSE	P08920 mus musculu
25	30	73.2	344	CD2_RAT	P08921 rattus norv
26	30	73.2	347	CD2_HORSE	P37998 equus cabal
27	30	73.2	354	ACOD_MESAU	O64420 mesocricetu
28	30	73.2	355	ACOD_MOUSE	P13516 mus musculu
29	30	73.2	358	ACOD2_MOUSE	P13011 mus musculu
30	30	73.2	358	ACOD_RAT	P07308 rattus norv
31	30	73.2	359	ACOD_BOVIN	Q9tt94 bos taurus
32	30	73.2	359	ACOD_HUMAN	O00767 homo sapien
33	30	73.2	359	ACOD_SHEEP	O62849 ovils aries

34	30	73.2	377	1	TGT_BRUME	Q8yhb2 mycoplasma
35	30	73.2	384	1	Y039_MYCPN	P75063 mycoplasma
36	30	73.2	448	1	HGD_RALSO	O8xr20 ralstonia s
37	30	73.2	453	1	HGD_RHIME	Q8x4f5 rhizobium m
38	30	73.2	457	1	HGD_RHILO	Q98334 rhizobium l
39	30	73.2	469	1	GLNA_PROVU	P28786 proteus vul
40	30	73.2	492	1	NMT_ASFPU	Q9uvx3 aspergillus
41	30	73.2	495	1	MLP2_DROME	Q24400 drosophila
42	30	73.2	623	1	MUTL_BRUME	Q8ybt4 streptomyce
43	30	73.2	624	1	DNAA_STRCH	Q9zh75 streptomyce
44	30	73.2	677	1	SKD3_MOUSE	Q06649 mus musculu
45	30	73.2	744	1	LCF2_YEAST	P39518 saccharomyc

ALIGNMENTS

RESULT 1
FIBB_CANFA STANDARD; PRT; 31 AA.
AC P02677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=76081726; PubMed=1198547;
RA Birken S., Wilner G.D., Canfield R.E.;
RT "Studies of the structure of canine fibrinogen."
RL Thromb. Res. 7:599-610(1975).
RN [2]
RP SEQUENCE OF 1-19.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [3]
RP SEQUENCE OF 1-19.
RX MEDLINE=69066367; PubMed=5727635;
RA Krajewski T., Blomback B.;
RT "The location of tyrosine-O-sulphate in fibrinopeptides."
RL Acta Chem. Scand. 22:1339-1346(1968).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; A03123; A03123.
DR PIR; A05297; A05297.
DR InterPro; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 19 FIBRINOPEPTIDE B.
FT CHAIN 20 >31 FIBRINOGEN BETA CHAIN.
FT MOD_RES 2 2 SULFATION (IN B[2] CHAIN).
FT MOD_RES 3 3 SULFATION (IN B[1] & B[2] CHAINS).
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3731 MW; A043727257698156 CRC64;
Query Match 100.0%; Score 41; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDK 7

Db 11111111
20 GHRPLDK 26

RESULT 2

FIBB_HUMAN STANDARD; PRT; 491 AA.

AC P02675;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].

GN FGB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-91344740; PubMed-2102623;

RA Chung D.W., Harris J.E., Davie E.W.;

RT "Nucleotide sequences of the three genes coding for human fibrinogen.";

RL Adv. Exp. Med. Biol. 281:39-48(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-83283433; PubMed-6688356;

RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;

RT "Characterization of complementary deoxyribonucleic acid and genomic deoxyribonucleic acid for the beta chain of human fibrinogen.";

RL Biochemistry 22:3244-3250(1983).

RN [3]

RP SEQUENCE FROM N.A.

RA Chung D.W., Harris J.E., Davie E.W.;

RT "Nucleotide sequences of the three genes coding for human fibrinogen.";

RL (In) Liu C.Y., Chien S. (eds.);

RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48, Plenum Press, New York (1991).

RN [4]

RP SEQUENCE FROM N.A., AND VARIANTS SER-100; HIS-170; LEU-265 AND LYS-478.

RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.

RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;

RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural variants.";

RL (In) Peeters H. (eds.);

RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56, Pergamon Press, Oxford (1980).

RN [6]

RP SEQUENCE OF 31-491.

RX MEDLINE-79124640; PubMed-420779;

RA Watt K.W.K., Takagi T., Doolittle R.F.;

RT "Amino acid sequence of the beta chain of human fibrinogen.";

RL Biochemistry 18:58-76(1979).

RN [7]

RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.

RX MEDLINE-76225080; PubMed-936108;

RA Blomback B., Hessel B., Hogg D.;

RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";

RL Thromb. Res. 8:639-658(1976).

RN [8]

RP SEQUENCE OF 1-38 FROM N.A.

RX MEDLINE-87146483; PubMed-3029722;

RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z., Marguerie G.;

RT "Characterization of the 5'-flanking region for the human fibrinogen beta gene.";

RL Nucleic Acids Res. 15:1615-1625(1987).

RN [9]

RP SEQUENCE OF 31-44.

RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;

RT "Studies on fibrinopeptides from primates.";

RL Acta Chem. Scand. 19:1788-1789(1965).

RN [10]

RP REVIEW, AND DISULFIDE BONDS.

RX MEDLINE-83254370; PubMed-6575689;

RA Henschen A., Lottspeich F., Kehl M., Southan C.;

RT "Covalent structure of fibrinogen.";

RL Ann. N.Y. Acad. Sci. 408:28-43(1983).

RN [11]

RP DISULFIDE BONDS.

RX MEDLINE-77245999; PubMed-891553;

RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;

RT "Primary structure of human fibrinogen. Characterization of disulfide-containing cyanogen-bromide fragments.";

RL Eur. J. Biochem. 77:595-610(1977).

RN [12]

RP DISULFIDE BONDS.

RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A., Casman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;

RT "The structures of fibrinogen and fibrin.";

RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K., Neurath H. (eds.);

RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172, Pergamon Press, New York (1978).

RN [13]

RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.

RX MEDLINE-84305751; PubMed-6383194;

RA Doolittle R.F.;

RT "Fibrinogen and fibrin.";

RL Annu. Rev. Biochem. 53:195-229(1984).

RN [14]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.

RX MEDLINE-97472408; PubMed-9333233;

RA Spraggon G., Everse S.J., Doolittle R.F.;

RT "Crystal structures of fragment D from human fibrinogen and its crosslinked counterpart from fibrin.";

RL Nature 389:455-462(1997).

RN [15]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.

RX MEDLINE-98292395; PubMed-9628725;

RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;

RT "Crystal structure of fragment double-D from human fibrin with two different bound ligands.";

RL Biochemistry 37:8637-8642(1998).

RN [16]

RP X-RAY CRYSTALLOGRAPHY.

RX MEDLINE-99175089; PubMed-10074346;

RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;

RT "Conformational changes in fragments D and double-D from human fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";

RL Biochemistry 38:2941-2946(1999).

RN [17]

RP VARIANT BALTIMORE-2.

RX MEDLINE-89058942; PubMed-3194892;

RA Schmeizer C.H., Ebert R.F., Bell W.R.;

RT "A polymorphism at B beta 448 of fibrinogen identified during structural studies of fibrinogen Baltimore II.";

RL Thromb. Res. 52:173-177(1988).

RN [18]

RP VARIANT ISE.

RX MEDLINE-91208409; PubMed-2018836;

RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K., Asakura S., Shirakawa S.;

RT "A new congenital abnormal fibrinogen Ise characterized by the replacement of B beta glycine-15 by cysteine.";

RL Blood 77:1958-1963(1991).

RN [19]

RP VARIANT NAPLES.

RX MEDLINE-92340664; PubMed-1634610;

RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;

RT "Molecular basis of fibrinogen Naples associated with defective
 RT thrombin binding and thrombophilia. Homozygous substitution of B beta
 RL 68 Ala-->Thr."; J. Clin. Invest. 90:238-244(1992).
 RN [20]
 RP VARIANTS IJMUDDEN AND NIJMEGEN.
 RX MEDLINE-92228809; PubMed-1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens IJMUDDEN (B beta Arg14-->Cys) and NIJMEGEN (B
 RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
 RT complexes."; Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 RL [21]
 RN VARIANT NEW YORK-1.
 RP MEDLINE-85157605; PubMed-3156856;
 RX Liu C.Y., Koehn J.A., Morgan F.J.;
 RA "Characterization of fibrinogen New York 1. A dysfunctional
 RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RT exon 2 of the gene."; J. Biol. Chem. 260:4390-4396(1985).
 RL [22]
 RN FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
 CC ENDS OF THE ALPHA CHAINS.
 CC -1- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL; J00129; AAA52429.1; -;
 CC EMBL; J00131; AAA98115.1; -;
 CC EMBL; J00130; AAA98115.1; JOINED.
 CC EMBL; J00132; AAA98116.1; -;
 CC EMBL; J00133; NOT_ANNOTATED_CDS.
 CC EMBL; AF386026; AAK62470.1; -;
 CC EMBL; X05018; CAA28674.1; -;
 CC EMBL; M64983; AAA18024.2; -;
 CC EMBL; M26877; AAA52445.1; -;
 CC EMBL; M26876; AAA52445.1; JOINED.

Query Match 100.0%; Score 41; DB 1; Length 491;
 Best Local Similarity 100.0%; Pred. No. 0.39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
 Db 45 GHRPLDK 51
 |||||

RESULT 3
 FIBB_BOVIN STANDARD; PRT; 468 AA.
 ID FIBB_BOVIN

AC P02676;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN FGB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-4.
 RA Blomback B., Doolittle R.F.;
 RT "The sequence of amino acids at the N-terminal end of bovine
 RL fibrinopeptide B."; Acta Chem. Scand. 17:1816-1819(1963).
 RN [2]
 RP SEQUENCE OF 5-21.
 RA Sjoquist J., Blomback B., Wallen P.;
 RT "Amino acid sequence of bovine fibrinopeptides."; Ark. Kemi 16:425-436(1960).
 RN [3]
 RP SEQUENCE OF 22-53.
 RX MEDLINE-79164394; PubMed-434821;
 RA Martinelli R.A., Ingalls A.S., Rubira M.R., Hageman T.C.,
 RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;
 RT "Amino acid sequences of portions of the alpha and beta chains of
 RL bovine fibrinogen."; Arch. Biochem. Biophys. 192:27-32(1979).
 RN [4]
 RP SEQUENCE OF 44-468 FROM N.A.
 RX MEDLINE-81199473; PubMed-6262803;
 RA Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
 RT "Characterization of a cDNA clone coding for the beta chain of bovine
 RL fibrinogen."; Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC
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 CC
 CC EMBL; V00110; CAA23444.1; -;
 CC PIR; A03122; FGBOB.
 CC HSPSP; P02675; IFZA.
 CC InterPro; IPR002181; Fibrinogen_C.
 CC Pfam; PF00147; fibrinogen_C; 1.
 CC SMART; SM00186; FGB; 1.
 CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 CC Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
 FT PEPTIDE 1 21 FIBRINOPEPTIDE B.
 FT CHAIN 22 468 FIBRINOGEN BETA CHAIN.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 6 6 SULFATION.
 FT SITE 21 22 CLEAVAGE (BY THROMBIN; RELEASE


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FT DISULFID 72 72 FIBRINOPEPTIDE B).
FT DISULFID 83 83 INTERCHAIN (WITH ALPHA).
FT DISULFID 87 87 INTERCHAIN (WITH ALPHA).
FT DISULFID 200 200 INTERCHAIN (WITH GAMMA).
FT DISULFID 204 204 INTERCHAIN (WITH ALPHA).
FT DISULFID 208 293 INTERCHAIN (WITH GAMMA).
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 401 414 BY SIMILARITY.
FT CARBOHYD 371 371 N-LINKED (GLCNAC... ) (PROBABLE).
SQ SEQUENCE 468 AA; 53340 MW; 2DED42F443AA4B37 CRC64;

Query Match 87.8%; Score 36; DB 1; Length 468;
Best Local Similarity 85.7%; Pred. No. 4.3; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
    |||||
Db 22 GHRPYDK 28

RESULT 4
FIBB_CHICK STANDARD; PRT; 463 AA.
AC Q02020;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
DE (Fragment).
GN FGB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE=91182745; PubMed=2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
RT cleavage site.";
RL Biochemistry 30:3290-3294(1991).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC
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CC
CC -----
CC ENBL: M58514; AAA48770.1; -.
CC PIR: A38463; A38463.
CC HSP: P02675; IEFZ.
CC InterPro: IPR002181; Fibrinogen_C.
CC Pfam: PF00147; fibrinogen_C; 1.
CC SMART: SM00186; FGB; 1.
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
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KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
FT NON_TER 1 1 FIBRINOPEPTIDE B.
FT PEPTIDE <1 17 FIBRINOGEN BETA CHAIN.
FT CHAIN 18 463 SULFATION (BY SIMILARITY).
FT MOD_RES 5 5 CLEAVAGE (BY THROMBIN; RELEASE
FT SITE 17 18 FIBRINOPEPTIDE B).
FT DISULFID 69 69 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 84 84 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 197 197 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 201 201 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 205 289 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 397 410 BY SIMILARITY.
FT CARBOHYD 367 367 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 463 AA; 52678 MW; 2044CD49BA79EC7B CRC64;

Query Match 85.4%; Score 35; DB 1; Length 463;
Best Local Similarity 100.0%; Pred. No. 6.9; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
    |||||
Db 19 HRPLDK 24

RESULT 5
FIBB_RAT STANDARD; PRT; 479 AA.
AC P14480;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN FGB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95143386; PubMed=7841303;
RA Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.;
RT "Cloning of the complete coding sequence of rat fibrinogen B beta
RT chain cDNA: interspecies conservation of fibrin beta 15-42 primary
RT structure.";
RL Blood Coagul. Fibrinolysis 5:487-496(1994).
RP [2]
RP SEQUENCE OF 1-26 FROM N.A.
RX MEDLINE=84194000; PubMed=6232608;
RA Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
RT "Potential basis for regulation of the coordinately expressed
RT fibrinogen genes: homology in the 5' flanking regions.";
RP Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
RN [3]
RP SEQUENCE OF 19-32.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [4]
RP SEQUENCE OF 183-479 FROM N.A.
RX MEDLINE=89378771; PubMed=2673932;
RA Eastman E.M., Gilula N.B.;
RT "Cloning and characterization of a cDNA for the B beta chain of rat
RT fibrinogen: evolutionary conservation of translated and
RT 3'-untranslated sequences.";
RL Gene 79:151-158(1989).
RN [5]
RP SEQUENCE OF 425-479 FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=87134033; PubMed=3817019;
```


RA Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 RT liver regeneration";
 RL Exp. Cell Res. 169:47-56(1987).
 CC -|- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -|- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -|- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 CC -|- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 DR EMBL: U05675; AAA64866.1; -
 DR EMBL: M27220; AAA41160.1; -
 DR EMBL: K01336; AAA98625.1; -
 DR EMBL: M35602; AAA41159.1; -
 DR PIR: A05299; A05299.
 DR PIR: PE0010; PE0010.
 DR HSP: P02675; 1F2E.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00314; FIBRIN_AG_C_DOMAIN; 1.
 DR Blood coagulation; Plasma; Glycoprotein; Signal.
 KW SIGNAL 1 18
 FT CHAIN 19 479
 FT PEPTIDE 19 32
 FT DISULFID 211 211
 FT FIBRINOGEN BETA CHAIN.
 FT FIBRINOPEPTIDE B. WITH THE ALPHA CHAIN)
 FT (BY SIMILARITY).
 FT INTERCHAIN (WITH THE GAMMA CHAIN)
 FT INTERCHAIN (WITH THE GAMMA CHAIN)
 FT (BY SIMILARITY).
 FT BY SIMILARITY).
 FT BY SIMILARITY).
 FT BY SIMILARITY).
 FT BY SIMILARITY).
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT LSI -> ILS (IN REF. 3).
 FT L -> Q (IN REF. 5).
 FT S -> T (IN REF. 5).
 FT S -> A (IN REF. 5).
 FT R -> K (IN REF. 5).
 FT V -> F (IN REF. 5).
 SQ SEQUENCE 479 AA; 54303 MW; EC8C6DB77C3E0EC0 CRC64;

Query Match 85.4%; Score 35; DB 1; Length 479;
 Best Local Similarity 71.4%; Pred. No. 7.2;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

DB 33 GHRPVDK 39

RESULT 6

EF5_MOUSE STANDARD; PRT; 560 AA.
 AC 064355;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Embryonal Fyn-associated substrate (SRC-interacting protein)
 DE (Signal integrating protein).
 GN EFS OR SIN.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF TYR-253.
 RC TISSUE-EMBRYO;
 RX MEDLINE-96249382; PubMed-8647432;
 RA Alexandropoulos K., Baltimore D.;
 RT "Coordinate activation of c-Src by SH3- and SH2-binding sites on a
 RT novel p130Cas-related protein, Sin.";
 RL Genes Dev. 10:1341-1355(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NIH Swiss; TISSUE-Embryo;
 RX MEDLINE-96112635; PubMed-8570184;
 RA Ishino M., Ohba T., Sasaki H., Sasaki T.;
 RT "Molecular cloning of a cDNA encoding a phosphoprotein, Efs, which
 RT contains a Src homology 3 domain and associates with Fyn.";
 RL Oncogene 11:2331-2338(1995).
 CC -|- FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL COORDINATING ROLE
 CC FOR TYROSINE-KINASE-BASED SIGNALING RELATED TO CELL ADHESION. MAY
 CC SERVE AS AN ACTIVATOR OF SRC AND A DOWNSTREAM EFFECTOR. INTERACTS
 CC WITH THE SH3 DOMAIN OF FYN AND WITH CRK, SRC, AND YES.
 CC -|- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER LEVELS FOUND IN
 CC PLACENTA AND EMBRYO. LOWER LEVELS FOUND IN LIVER, BRAINSTEM,
 CC MUSCLE AND LUNG. NO EXPRESSION IN LIVER AND INTESTINE.
 CC -|- DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING
 CC MULTIPLE POTENTIAL SH2-BINDING SITES AND A C-TERMINAL DOMAIN
 CC CONTAINING A DIVERGENT HELIX-LOOP-HELIX (HLH) MOTIF. THE SH2-
 CC BINDING SITES PUTATIVELY BIND CRK, NCK AND ABL SH2 DOMAINS.
 CC -|- DOMAIN: THE SH3-BINDING SITES BIND TO THE SRC SH3 DOMAIN ARE
 CC REQUIRED FOR INTERACTION WITH CRK AND ARE IMPLICATED IN PROMOTION
 CC OF SERUM RESPONSE ELEMENT (SRE) ACTIVATION. THE SH3 DOMAIN
 CC INTERACTS WITH FOCAL ADHESION KINASE 1.
 CC -|- PTM: PHOSPHORYLATED ON MULTIPLE TYROSINE RESIDUES. PHOSPHORYLATED
 CC ON TYROSINES BY FYN AND SRC.
 CC -|- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -|- SIMILARITY: BELONGS TO THE CAS FAMILY.
 CC -----
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 CC -----
 DR EMBL: U57686; AAB02246.1; -
 DR EMBL: U28728; RAC52340.1; -
 DR HSP: Q60631; IGBQ.
 DR MGD; MGI:105311; Efs.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00018; SH3; 1.
 DR ProDom: PD000066; SH3; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00002; SH3; 1.
 DR Phosphorylation; SH3 domain; SH3-binding; Cell adhesion.
 KW DOMAIN 5 68
 FT SITE 304 310
 FT SITE 334 340
 FT SITE 335 341
 FT DOMAIN 437 487
 FT MOD_RES 253 253
 FT MUTAGEN 253 253
 SQ SEQUENCE 560 AA; 58970 MW; D22A66F51BB264A8 CRC64;
 Y->F: DIMINISH THE ABILITY TO INDUCE SRC-
 MEDIATED ACTIVATION OF LUCIFERASE.

Query Match 78.0%; Score 32; DB 1; Length 560;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

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Db          393 GSRPLDK 399
RESULT 7
HD4A_CHICK STANDARD; PRT; 1080 AA.
AC P83038;
DT 15-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Histone deacetylase 4 (HD4).
GN HDAC4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Takechi S., Azuma R., Nakayama T.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
CC THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
CC HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
CC REGULATION; CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
CC SIMILARITY). REPRESENTS TRANSCRIPTION (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
CC FAMILY. HD SUBFAMILY 2.
CC -----
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CC -----
DR EMBL; AB052839; BAB60957.1; -
DR InterPro; IPR000286; Hist_deacetylase.
DR Pfam; PF00850; Hist_deacetyl; 1.
DR PRINTS; PR01270; HDASUPER.
KW Hydrolase; Nuclear protein; Transcription regulation; Repressor.
FT DOMAIN 651 1080
SQ SEQUENCE 1080 AA; 119467 MW; B6416E2C43F1428C CRC64;

Query Match 78.0%; Score 32; DB 1; Length 1080;
Best Local Similarity 71.4%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 619 GHRPLSR 625

RESULT 8
HD4A_HUMAN STANDARD; PRT; 1084 AA.
AC P56524; Q9UND6;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Histone deacetylase 4 (HD4) (HA6116).
GN HDAC4 OR KIAA0288.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Grozinger C.M., Hassig C.A., Schreiber S.L.;
RL MEDLINE=99238449; PubMed=10220385;

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RT "Three proteins define a class of human histone deacetylases related
RL to yeast Hda1p.";
RN Proc. Natl. Acad. Sci. U.S.A. 96:4868-4873(1999).
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97323006; PubMed=9179496;
RA Ohara O., Nagase T., Ishikawa K.-I., Nakajima D., Ohira M.,
RA Seki N., Nomura N.;
RT "Construction and characterization of human brain cDNA libraries
RT suitable for analysis of cDNA clones encoding relatively large
RT proteins.";
RL DNA Res. 4:53-59(1997).
RN [3]
RP REVISIONS TO N-TERMINUS.
RA Ohara O., Nagase T., Ishikawa K.-I., Nakajima D., Ohira M.,
RA Seki N., Nomura N.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99455038; PubMed=10523670;
RA Wang A.H., Bertos N.R., Vezmar M., Pelletier N., Crosato M.,
RA Heng H.H., Th'ng J., Han J., Yang X.J.;
RT "HDAC4, a human histone deacetylase related to yeast Hda1, is a
RT transcriptional corepressor.";
RL Mol. Cell. Biol. 19:7816-7827(1999).
CC -1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
CC THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
CC HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
CC REGULATION; CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
CC SIMILARITY). REPRESENTS TRANSCRIPTION.
CC -1- SUBUNIT: INTERACTS WITH MEF2C.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
CC FAMILY. HD SUBFAMILY 2.
CC -----
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CC -----
DR EMBL; AF132607; AAD29046.1; -
DR EMBL; AB006626; BAA22957.2; ALT_INIT.
DR Genew; HGNC:14063; HDAC4.
DR MIM; 605314; -
DR InterPro; IPR000286; Hist_deacetylase.
DR Pfam; PF00850; Hist_deacetyl; 1.
DR PRINTS; PR01270; HDASUPER.
KW Hydrolase; Nuclear protein; Transcription regulation; Repressor.
FT DOMAIN 655 1084
SQ SEQUENCE 1084 AA; 119069 MW; DF5F30DA9C4295FD CRC64;

Query Match 78.0%; Score 32; DB 1; Length 1084;
Best Local Similarity 71.4%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 623 GHRPLSR 629

RESULT 9
MBP_RABIT
ID MBP_RABIT STANDARD; PRT; 168 AA.
AC P35274;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Myelin basic protein (MBP) (Myelin A1 protein) (Myelin P1 protein).

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GN MBP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RN PRELIMINARY SEQUENCE.
 RC TISSUE=Sciatic nerve;
 RX MEDLINE=73190037; PubMed=4662101;
 RA Brostoff S.W., Eylar E.H.;
 RT "The proposed amino acid sequence of the P1 protein of rabbit sciatic
 RL nerve myelin.";
 RN Arch. Biochem. Biophys. 153:590-598(1972).
 RN [2]
 RP SEQUENCE OF 45-86.
 RA Shapira R., McNeally S.S., Chou F., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RL sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RN J. Biol. Chem. 246:4630-4640(1971).
 RN [3]
 RP PHOSPHORYLATION.
 RX MEDLINE=83108902; PubMed=6185481;
 RA Martenson R.E., Law M.J., Deibler G.E.;
 RT "Identification of multiple *in vivo* phosphorylation sites in rabbit
 RL myelin basic protein.";
 RN J. Biol. Chem. 258:930-937(1983).
 CC -|- FUNCTION: Is, with PLP, the most abundant protein component of the
 CC myelin membrane in the CNS. Has a role in both the formation and
 CC stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 CC function in the assembly of an optimized, biochemically functional
 CC myelin membrane (By similarity).
 CC -|- SUBUNIT: Homodimer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -|- TISSUE SPECIFICITY: Found in both the central and the peripheral
 CC nervous system.
 CC -|- PTM: As in other animals, several charge isomers may be produced
 CC as a result of optional posttranslational modifications, such as
 CC phosphorylation of serine or threonine residues, deamidation of
 CC glutamine or asparagine residues, citrullination and methylation
 CC of arginine residues.
 CC -|- PTM: The N-terminus is blocked.
 CC -|- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 DR PIR: B92087; B92087.
 DR HSP: P02686; IQCL.
 DR InterPro: IPR000348; Myelin_BP.
 DR Pfam: PF01669; Myelin_MBP; 1.
 DR PRINTS: PR00212; MYELINBP.
 DR PROSITE: PS00569; MYELIN_MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Citrullination; Autoimmune encephalomyelitis.
 FT DOMAIN 45 86
 FT INDUCES EXPERIMENTAL AUTOIMMUNE
 FT ENCEPHALOMYELITIS (EAE).
 FT ACETYLATION (PROBABLE).
 FT PHOSPHORYLATION.
 FT CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT PHOSPHORYLATION.
 FT PHOSPHORYLATION.
 FT PHOSPHORYLATION.
 FT PHOSPHORYLATION (PROBABLE).
 FT DEAMIDATION (PARTIAL) (BY SIMILARITY).
 FT METHYLATION (MONO- OR DI-).
 FT CITRULLINATION.
 FT CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT CITRULLINATION (PARTIAL) (BY SIMILARITY).
 FT PHOSPHORYLATION (PARTIAL) (BY
 FT SIMILARITY).
 FT PHOSPHORYLATION.
 FT CITRULLINATION (BY SIMILARITY).
 FT CITRULLINATION (BY SIMILARITY).
 FT S -> G (IN REF. 2).
 SQ SEQUENCE 168 AA; 18217 MW; EC3C97ACD2C08EA6 CRC64;

Query Match

75.6%; Score 31; DB 1; Length 168;

Best Local Similarity 71.4%; Pred. No. 16;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB 75 GHRPQDE 81
 RESULT 10
 MBP_BOVIN STANDARD; PRT; 169 AA.
 ID MBP_BOVIN QNTSA6; QNTS63; O9BGM8;
 AC P02687; QNTSA6 (Rel. 01, Created);
 DT 21-JUL-1986 (Rel. 01, Last sequence update);
 DT 21-JUL-1986 (Rel. 01, Last annotation update);
 DE Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa microtubule
 GN stabilizing protein).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE.
 RX MEDLINE=72007306; PubMed=5096093;
 RA Eylar E.H., Brostoff S.W., Hashim G., Caccam J., Burnett P.;
 RT "Basic A1 protein of the myelin membrane. The complete amino acid
 RL sequence.";
 RN J. Biol. Chem. 246:5770-5784(1971).
 RN [2]
 RN REVISION.
 RX MEDLINE=74070688; PubMed=4129204;
 RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;
 RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";
 RN J. Biol. Chem. 249:559-567(1974).
 RN [3]
 RN SEQUENCE OF 4-56 FROM N.A.
 RA Pietrowski D., Medugorac I., Foerster M.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RL sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RN J. Biol. Chem. 246:4630-4640(1971).
 RN [4]
 RN SEQUENCE OF 43-87.
 RA Shapira R., McNeally S.S., Chou F.C.-H., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RL sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RN J. Biol. Chem. 246:4630-4640(1971).
 RN [5]
 RN SEQUENCE OF 38-58 AND 119-141.
 RC TISSUE=Brain;
 RX MEDLINE=93003019; PubMed=1382581;
 RA Pirollet F., Derancourt J., Haiech J., Job D., Margolis R.L.;
 RT "Ca(2+)-calmodulin regulated effectors of microtubule stability in
 RL bovine brain.";
 RN Biochemistry 31:8849-8855(1992).
 RN [6]
 RN SEQUENCE OF 30-42; 74-89 AND 114-129.
 RX MEDLINE=96107211; PubMed=8530487;
 RA Prasad K., Barouch W., Martin B.M., Greene L.E., Eisenberg E.;
 RT "Purification of a new clathrin assembly protein from bovine brain
 RL coated vesicles and its identification as myelin basic protein.";
 RN J. Biol. Chem. 270:30551-30556(1995).
 RN [7]
 RN SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.
 RX MEDLINE=70178977; PubMed=5442707;
 RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;
 RT "Experimental allergic encephalomyelitis: synthesis of
 RL disease-inducing site of the basic protein.";
 RN Science 168:1220-1223(1970).
 RN [8]
 RN METHYLATION.
 RX MEDLINE=71153946; PubMed=4994464;
 RA Brostoff S.W., Eylar E.H.;

FT	MOD_RES	23	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	23	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	29	PHOSPHORYLATION (IN C4, C5 AND C6).
FT	MOD_RES	54	PHOSPHORYLATION (BY MAPK) (IN C3, C4, C5 AND C6).
FT	MOD_RES	97	DEAMINATION (IN C5).
FT	MOD_RES	102	METHYLATION (MONO- OR DI-).
FT	MOD_RES	106	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	114	DEAMINATION (IN C2).
FT	MOD_RES	129	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	146	PHOSPHORYLATION (IN C4 AND C6).
FT	MOD_RES	158	PHOSPHORYLATION (IN C3, C5 AND C6).
FT	MOD_RES	160	CITRULLINATION (PARTIAL) (BY SIMILARITY).
FT	MOD_RES	164	PHOSPHORYLATION (IN C3, C5 AND C6).
FT	MOD_RES	169	CITRULLINATION (PROBABLE).
SQ	SEQUENCE	169 AA; 18323 MW; 8E1157B7A1978484 CRC64;	

Query Match 75.6%; Score 31; DB 1; Length 169;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	GHRPLDK 7	
		:	
Db	76	GHRPQDE 82	

RESULT 11
PCP_BACSU STANDARD; PRT; 215 AA.
AC P28618;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pyridone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolinyl-peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase).
DE PCP.
GN Bacillus subtilis.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=92339527; PubMed=13530326;
RA Awade A., Cleuziat P., Gonzales T., Robert-Baudouy J.;
RT "Characterization of the pcg gene encoding the pyrrolidone carboxyl peptidase of Bacillus subtilis.";
RL FEBS Lett. 305:67-73(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=95219079; PubMed=7704254;
RA Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
RT "Determination of a 21548 bp nucleotide sequence around the 24 degrees region of the Bacillus subtilis chromosome.";
RL Microbiology 141:269-275(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I.; Albertini A.M., Alloni G., Azevedo V., Bortner M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L., Joris B., Karamata D., Kashara Y., Klaer-Blaichard M., Klein C., Kobayashi Y., Koeter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinou S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogivara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Pujic C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta P., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanaka S., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassaroni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [4]
RP SEQUENCE OF 1-18, AND CHARACTERIZATION.
RX MEDLINE=93139164; PubMed=1362573;
RA Gonzales T., Awade A., Besson C., Robert-Baudouy J.;
RA "Purification and characterization of recombinant pyrrolidone carboxyl
RT peptidase of Bacillus subtilis.";
RT J. Chromatogr. A 584:101-107(1992).
RL J. FUNCTION: REMOVES 5-OXOPROLINE FROM VARIOUS PENULTIMATE AMINO ACID
CC RESIDUES EXCEPT L-PROLINE.
CC -|- CATALYTIC ACTIVITY: 5-oxoprol-yl-peptide + H(2)O -> 5-oxoproline +
CC peptide.
CC -|- SUBUNIT: HOMOTETRAMER.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C15.
CC
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CC
CC EMBL; X66034; CAA46833.1; -
CC EMBL; D30808; BAA06485.1; -
CC EMBL; A25847; CAA01777.1; -
CC EMBL; Z99105; CAB12059.1; -
CC PIR; S23432; S23432.
CC HSP; P46107; IAUG.
CC MEROPS; C15.001; -
CC Subtilist; BG10873; pcp.
CC InterPro; IPR000816; Peptidase_C15.
CC Pfam; PF01470; Peptidase_C15; 1.
CC ProDom; PD008480; Peptidase_C15; 1.
CC TIGRFams; TIGR00504; pyro_pdae; 1.
CC PROSITE; PS01333; PYRASE_GLU; 1.
CC PROSITE; PS01334; PYRASE_CYS; 1.
CC Hydrolase; Thiol protease; Complete proteome.
FT ACT_SITE 81 81 BY SIMILARITY.
FT ACT_SITE 144 144 BY SIMILARITY.
FT ACT_SITE 168 168 BY SIMILARITY.
SQ SEQUENCE 215 AA; 23774 MW; A8804117BCCFE24 CRC64;

Query Match 75.6%; Score 31; DB 1; Length 215;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 97 GHQPID 103

RESULT 12
MRAW_ZYMO
ID MRAW_ZYMO STANDARD; PRT; 333 AA.
AC Q9RE09; Q9RNM0;
DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE S-adenosyl-methyltransferase mraw (EC 2.1.1.-).
GN MRAW OR ZM10RF5 OR ZM16ORF1.
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RA Um H.W., Kang H.S.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase
CC activity (by similarity).
CC -|- SIMILARITY: BELONGS TO THE MRAW FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF179611; AAD53943.1; -
CC EMBL; AF213822; AAP23786.1; -
CC InterPro; IPR002903; Bac_Metrnfrse.
CC Pfam; PF01795; Methyltransf_5; 1.
CC ProDom; PD004685; Bac_Metrnfrse; 1.
CC TIGRFams; TIGR00006; UPF0117; 1.
CC Transferase; Methyltransferase.
KW SEQUENCE 333 AA; 37347 MW; A090E25F84587F79 CRC64;
SQ

Query Match 75.6%; Score 31; DB 1; Length 333;
Best Local Similarity 71.4%; Pred. No. 34;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 192 GYRPFDK 198

RESULT 13
TRMA_PSEFL
ID TRMA_PSEFL STANDARD; PRT; 363 AA.
AC O9RHS9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE TRNA (Uracil-5-)-methyltransferase (EC 2.1.1.35) (trna(M-5-U54)-
DE methyltransferase) (RUMT).
GN TRMA.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=No. 33;
RX MEDLINE=20069636; PubMed=10601212;
RA Idei A., Kawai E., Akatsuka H., Omori K.;
RT "Cloning and characterization of the Pseudomonas fluorescens ATP-
RT binding cassette exporter, HasDEF, for the heme acquisition protein
RT HasA.";
RL J. Bacteriol. 181:7545-7551(1999).
CC -|- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position
CC 54 (M-5-U54) in all tRNA (By similarity).
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA -> S-adenosyl-L-
CC homocysteine + tRNA containing thymine.
CC -|- SIMILARITY: BELONGS TO THE RNA M5U METHYLTRANSFERASE FAMILY. TRMA
CC SUBFAMILY.
CC

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 CC -----
 DR EMBL; AB023289; BAA88495.1; ..
 DR InterPro; IPR000051; SAM_bind.
 DR InterPro; IPR001566; TRMA.
 DR PROSITE; PS01230; TRMA_1; 1.
 DR PROSITE; PS01231; TRMA_2; FALSE NEG.
 KW Transferase; Methyltransferase; tRNA processing.
 FT DOMAIN 213 219 S-ADENOSYLMETHIONINE BINDING (BY
 FT ACT_SITE 321 321 BY SIMILARITY).
 FT SEQUENCE 363 AA; 41258 MW; 5B2F52954180AE38 CRC64;
 Query Match 75.6%; Score 31; DB 1; Length 363;
 Best Local Similarity 83.3%; Pred. No. 38;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 2 HRPDLK 7
 DB 127 HRPDLK 132
 |||||
 .RESULT 14
 TGT_SYNY3
 ID TGT_SYNY3 STANDARD; PRT; 374 AA.
 AC Q55983;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (tRNA-guanine
 DE transglycosylase) (Guanine insertion enzyme).
 GN TCT OR SLR0713.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=6590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166(1995).
 CC -1- FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-
 CC deazaguanine in tRNAs with GU(N) anticodons (CRNA-Asp, -Asn, -His
 CC and -Tyr). After this exchange, a cyclopentadiol moiety is
 CC attached to the 7-aminomethyl group of 7-deazaguanine, resulting
 CC in the hypermodified nucleoside queuosine (Q) (7-((4,5'-cis-
 CC dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine +
 CC guanine.
 CC -1- COFACTOR: BINDS AND REQUIRES ZINC FOR ACTIVITY. ALSO REQUIRES
 CC MAGNESIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; D64005; BAA10764.1; ..
 DR HSP; P28720; IPUD.

DR InterPro; IPR004803; Q.tRNA_tgt.
 DR InterPro; IPR002616; Que_tRNAtransf.
 DR Pfam; PF01702; TGT; 1.
 DR TIGRFAMS; TIGR00430; Q.tRNA_tgt; 1.
 DR TIGRFAMS; TIGR00449; tgt_general; 1.
 KW Queuosine biosynthesis; Transferase; Glycosyltransferase;
 KW tRNA processing; Zinc; Magnesium; Complete proteome.
 FT ACT_SITE 99 99 BY SIMILARITY.
 FT ACT_SITE 273 273 BY SIMILARITY.
 FT METAL 310 310 ZINC (BY SIMILARITY).
 FT METAL 312 312 ZINC (BY SIMILARITY).
 FT METAL 315 315 ZINC (BY SIMILARITY).
 FT METAL 341 341 ZINC (BY SIMILARITY).
 FT SEQUENCE 374 AA; 41498 MW; E8D65D266D6DCB24 CRC64;
 Query Match 75.6%; Score 31; DB 1; Length 374;
 Best Local Similarity 83.3%; Pred. No. 39;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 2 HRPDLK 7
 DB 303 HRPDLK 308
 |||||
 .RESULT 15
 THC2_METH
 ID THC2_METH STANDARD; PRT; 424 AA.
 AC O27617;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable thiamine biosynthesis protein thic 2.
 DE Thic2 OR MTH1576.
 GN Methanobacterium thermoautotrophicum.
 OS Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Frabnakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF THE HYDROMETHYLPIRIMIDINE
 CC (HMP) MOIETY OF THIAMINE (4-AMINO-2-METHYL-5-
 CC HYDROXYMETHYLPIRIMIDINE) (BY SIMILARITY).
 CC -1- PATHWAY: Thiamine biosynthesis.
 CC -1- SIMILARITY: BELONGS TO THE THIC FAMILY.
 CC -----
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 CC -----
 DR EMBL; AE000917; AAB86049.1; ..
 DR InterPro; IPR002817; Thic.
 DR Pfam; PF01964; Thic; 1.
 DR ProDom; PD007048; Thic; 1.
 DR TIGRFAMS; TIGR00190; thic; 1.
 KW Thiamine biosynthesis; Complete proteome.
 FT SEQUENCE 424 AA; 46314 MW; 13834EDE6B13B5BB CRC64;

Query Match 75.6%; Score 31; DB 1; Length 424;
Best Local Similarity 71.4%; Pred.No. 45;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
 |||
Db 267 GHMPLDQ 273

Search completed: June 16, 2003, 16:03:34
Job time : 7.06667 secs

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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:01:29 ; Search time 22.4 Seconds
(without alignments)
64.390 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41

Sequence: 1 GHRPLDK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPREMBL_21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	100.0	411	4 Q8W77	Q8W77 homo sapien
2	37	90.2	923	5 Q9VA50	Q9VA50 drosophila
3	36	87.8	201	16 Q92XY9	Q92XY9 rhizobium m
4	36	87.8	471	10 Q8SBA0	Q8SBA0 oryza sativ
5	36	87.8	735	10 Q9AE87	Q9AE87 oryza sativ
6	36	87.8	1490	10 Q9M1C7	Q9M1C7 arabidopsis
7	35	85.4	505	4 Q9HA50	Q9HA50 homo sapien
8	35	85.4	959	2 Q46583	Q46583 desulfovibr
9	35	85.4	1371	4 Q9Y2K2	Q9Y2K2 homo sapien
10	34	82.9	417	16 Q8R9G7	Q8R9G7 thermoanaer
11	34	82.9	673	3 Q94271	Q94271 schizosacch
12	34	82.9	795	10 Q9S1Z7	Q9S1Z7 arabidopsis
13	33	80.5	67	9 Q94MW0	Q94MW0 bacterioph
14	33	80.5	225	16 Q9RXW3	Q9RXW3 deinococcus
15	33	80.5	226	16 Q983T8	Q983T8 rhizobium l
16	33	80.5	244	2 Q93JU5	Q93JU5 pseudomonas

17	33	80.5	368	16 Q9KXQ8	Q9KXQ8 streptomyce
18	33	80.5	377	12 Q99FX0	Q99FX0 human papil
19	33	80.5	391	5 Q9VSB2	Q9VSB2 drosophila
20	33	80.5	717	12 Q9QP18	Q9QP18 gallid herp
21	33	80.5	1014	2 Q9RA53	Q9RA53 thermus the
22	33	80.5	1058	16 Q9PCW4	Q9PCW4 xylella fas
23	33	80.5	375	16 Q8XZJ5	Q8XZJ5 ralstonia s
24	32	78.0	409	10 Q9XEP2	Q9XEP2 sorghum bic
25	32	78.0	423	5 Q18847	Q18847 caenorhabdi
26	32	78.0	474	5 Q95RF0	Q95RF0 drosophila
27	32	78.0	474	5 Q9VMQ6	Q9VMQ6 drosophila
28	32	78.0	474	5 Q9VMQ3	Q9VMQ3 drosophila
29	32	78.0	476	16 Q50017	Q50017 mycobacteri
30	32	78.0	485	16 Q67746	Q67746 aquifex aeo
31	32	78.0	487	5 Q8SYF7	Q8SYF7 drosophila
32	32	78.0	490	5 Q9VSD0	Q9VSD0 drosophila
33	32	78.0	577	16 Q8XT98	Q8XT98 ralstonia s
34	32	78.0	611	10 Q9ZU34	Q9ZU34 arabidopsis
35	32	78.0	614	4 Q8WU14	Q8WU14 homo sapien
36	32	78.0	614	4 Q9NW41	Q9NW41 homo sapien
37	32	78.0	822	12 Q8U2I6	Q8U2I6 cercopithec
38	32	78.0	855	4 Q9NYK9	Q9NYK9 homo sapien
39	32	78.0	878	4 Q9UFU7	Q9UFU7 homo sapien
40	32	78.0	938	11 Q9JL72	Q9JL72 mus musculu
41	32	78.0	1123	4 Q9P2I9	Q9P2I9 homo sapien
42	31	75.6	104	2 Q9L500	Q9L500 bifidobacte
43	31	75.6	104	2 Q9L4Z6	Q9L4Z6 bifidobacte
44	31	75.6	104	2 Q9L504	Q9L504 bifidobacte
45	31	75.6	104	2 Q9L503	Q9L503 bifidobacte

ALIGNMENTS

RESULT 1

Q8W77	Q8W77	PRELIMINARY;	PRT;	411 AA.
ID	Q8W77	PRELIMINARY;	PRT;	411 AA.
AC	Q8W77	01-MAR-2002 (TREMREL. 20, Created)		
DT	01-MAR-2002	(TREMREL. 20, Last sequence update)		
DT	01-JUN-2002	(TREMREL. 21, Last annotation update)		
DE	Hypothetical 46.9 kDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC020762; AAH20762.1;			
DR	InterPro; IPR002181; Fibrinogen.C.			
DR	InterPro; IPR001019; Gprotein_alpha			
DR	Pfam; PF00147; fibrinogen_C; 1.			
DR	Pfam; PF00503; G-alpha; 1.			
DR	SMART; SM00186; FBC; 1.			
DR	SMART; SM00275; G-alpha; 1.			
KW	Hypothetical protein.			
SQ	SEQUENCE 411 AA; 46884 MW; 601E4E47F60E056 CRC64;			

Query Match 100.0%; Score 41; DB 4; Length 411;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7

|||||

Db 45 GHRPLDK 51

RESULT 2

Q9VA50 PRELIMINARY; PRT; 923 AA.

AC 09A50;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CG9713 protein.
 DE CG9713.
 OS Drosophila melanogaster (Fruit fly).
 GN Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacht J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-f., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003774; AAF57073.1;
 DR FlyBase; FBgn039793; CG9713.
 DR InterPro; IPR005123; 2OG-Fall_Oxy.
 DR Pfam; PF03171; 2OG-Fall_Oxy; 2.
 SQ SEQUENCE 923 AA; 105446 MW; 7EA45D9BB6E0C929 CRC64;
 Query Match 90.2%; Score 37; DB 5; Length 923;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDK 7
 DB 539 GHRPLEK 545
 RESULT 3
 Q92XY9
 ID Q92XY9 PRELIMINARY; PRT; 201 AA.
 AC Q92XY9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative transcriptional regulator.
 GN RAI099 OR SMA2008.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 GN Plasmid pSymA (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abolia A.P.,
 RA Barloy-Hudier F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 Sinorhizobium meliloti pSymA megaplasmid."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL; AE007296; AAK65757.1;
 DR InterPro; IPR001647; HTH_Tetr.
 DR Pfam; PF00440; tetr; 1.
 KW Plasmid; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 201 AA; 21500 MW; 447E9E9BF63EF551 CRC64;
 Query Match 87.8%; Score 36; DB 16; Length 201;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLD 6
 DB 175 GHRPLD 180
 RESULT 4
 Q8SBA0
 ID Q8SBA0 PRELIMINARY; PRT; 471 AA.
 AC Q8SBA0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 50.2 kDa protein.
 GN OSJNBAA042H09.17.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
 RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
 RA Tsittin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
 RA Valenzen S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
 RA Salzberg S.L., White O., Fraser C.M.;
 RT "Oryza sativa chromosome 10 BAC OSJNBAA0042H09 genomic sequence."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC079874; AAL79787.1;
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 50200 MW; 75D92E78D51937DD CRC64;
 Query Match 87.8%; Score 36; DB 10; Length 471;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLD 6
 DB 32 GHRPLD 37

RESULT 5

Q94E87
ID Q94E87 PRELIMINARY; PRT; 735 AA.
AC Q94E87
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE B1045D11.13 protein.
GN B1045D11.13.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:B1045D11.1";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003198; BAB61147.1;
DR InterPro; IPR001092; HLB_Basic.
DR InterPro; IPR002885; PPR.
DR Pfam; PF01535; PPR; 11.
DR TIGRFAMs; TIGR00756; PPR; 7.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 735 AA; 7989 MW; 540392FCBF125EF6 CRC64;

Query Match 87.8%; Score 36; DB 10; Length 735;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
| | | | |
DB 94 GHRPLD 99

RESULT 6

Q9M1C7
ID Q9M1C7 PRELIMINARY; PRT; 1490 AA.
AC Q9M1C7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Multi resistance protein homolog.
GN T209.140.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nyakatura G., Martmann B., Dauner D., Sterr W., Holland R., Quetier F.,
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
DR EMBL; AL138658; CAB75931.1; -.
DR HSSP; P13569; 1NBD.
DR InterPro; IPR003593; AAA_Artpase.
DR InterPro; IPR001140; ABCtransport.
DR InterPro; IPR003439; ABCtransport.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transport; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.

KW ATP-binding; Transport.
SQ SEQUENCE 1490 AA; 166455 MW; 237FCE03A3B4DA0F CRC64;

Query Match 87.8%; Score 36; DB 10; Length 1490;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
| | | | |
DB 1226 GHRPLD 1231

RESULT 7

Q9HA50
ID Q9HA50 PRELIMINARY; PRT; 505 AA.
AC Q9HA50
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CDNA FLJ12240 fls, clone MAMMA1001271.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK022302; BAB14006.1;
SQ SEQUENCE 505 AA; 54782 MW; 43BADEB48C0DFBE7 CRC64;

Query Match 85.4%; Score 35; DB 4; Length 505;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLD 7
| | | | |
DB 41 GHRPLD 47

RESULT 8

Q46583
ID Q46583 PRELIMINARY; PRT; 959 AA.
AC Q46583
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DcrH.
GN DCRH.
OS Desulfovibrio vulgaris (strain Hildenborough).
OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrionaceae;
OC Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE OF 605-727 FROM N.A.
RC STRAIN=HILDENBOROUGH;
RX MEDLINE=94117369; PubMed=8288529;
RA Deckers H.M., Voordouw G.;
RT "Identification of a large family of genes for putative chemoreceptor
RT proteins in an ordered library of the Desulfovibrio vulgaris
RL J. Bacteriol. 176:351-358(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HILDENBOROUGH;

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RX MEDLINE-96433451; PubMed-8836438;
RA Deckers H.M., Voordouw G.;
RT "the dcr gene family of Desulfovibrio: implications from the sequence
RT of dcrH and phylogenetic comparison with other mcp genes.";
RL Antonie Van Leeuwenhoek 70:21-29(1996).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN-HILDENBOROUGH;
RA Voordouw G.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U30319; AAB50497.1; -.
DR HSSP; P02942; 1QU7.
DR InterPro; IPR004089; Chmtaxis_transd.
DR InterPro; IPR002063; Hemerythrin.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF01814; Hemerythrin; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR ProDom; PD006099; Hemerythrin; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; MA; 1.
SQ SEQUENCE 959 AA; 104729 MW; 450550E840954D42 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 959;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDK 7
DB 513 HRPLDK 518

RESULT 9
-Q9Y2K2
ID Q9Y2K2 PRELIMINARY; PRT; 1371 AA.
AC Q9Y2K2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE KIAA0999 protein (Fragment).
GN KIAA0999.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=BRAIN;
RC SEQUENCE FROM N.A.
RX MEDLINE-99246063; PubMed=10231032;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB023216; BAA76843.2; -.
DR HSSP; Q03450; 1A06.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Serine/threonine-protein kinase.
FT NON_TER 1
SQ SEQUENCE 1371 AA; 149525 MW; F0FBA385B8226158 CRC64;

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Query Match 85.4%; Score 35; DB 4; Length 1371;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
DB 907 GHRPLSK 913

RESULT 10
-Q8R9G7
ID Q8R9G7 PRELIMINARY; PRT; 417 AA.
AC Q8R9G7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE UDP-N-acetylglucosamine enolpyruvyl transferase.
GN MUR2 OR TTE1644.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MB4T / JCM11007;
RX MEDLINE-21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013119; AAM24846.1; -.
KW Transferase; Complete proteome.
SQ SEQUENCE 417 AA; 45211 MW; 0A199EC2B104DC6E CRC64;

Query Match 82.9%; Score 34; DB 16; Length 417;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
DB 119 GHRPID 124

RESULT 11
-O94271
ID O94271 PRELIMINARY; PRT; 673 AA.
AC O94271;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Zinc finger protein.
GN SPBP857.23.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972H-;
RA Beck A., Reinhardt R., Lyne M., Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL032684; CAA21808.1; -.
DR InterPro; IPR001841; znf_ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; 2F_RING_1; 1.
KW Zinc-finger.
SQ SEQUENCE 673 AA; 76459 MW; 7317BDAD768FC883 CRC64;

Query Match 82.9%; Score 34; DB 3; Length 673;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;

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Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
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Db 160 GHPMDK 166

RESULT 12

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AC Q9SIZ7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE At2g22020 protein.
GN AT2G22020.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosidids II; Brassicales; Brassicaceae; Arabidopsis.
ON NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC007019; AAD20419.1; -
DR InterPro: IPR003878; SPRY_domain.
DR InterPro: IPR003877; SPRY_receptor.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00449; SPRY; 1.
SQ SEQUENCE 795 AA; 89006 MW; 07625DE69DBFE0D CRC64;

Query Match 82.9%; Score 34; DB 10; Length 795;

Best Local Similarity 71.4%; Pred. No. 1.2e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
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Db 41 GHRPLER 47

RESULT 13

Q94MWO PRELIMINARY; PRT; 67 AA.
AC Q94MWO;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ORF soc.2.
GN SOC.2.
OS Bacteriophage T6.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OC NCBI_TaxID=10666;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21353060; PubMed=11459968;
RA Mosig G., Gavin J., Luder A., Colowick N., Vo D.;

RT "Two recombination-dependent DNA replication pathways of bacteriophage
T4, and their roles in mutagenesis and horizontal gene transfer";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8306-8311(2001).
DR EMBL: AF374620; AAK66984.1; -
SQ SEQUENCE 67 AA; 8010 MW; D8C5AA79420D0A6 CRC64;

Query Match 80.5%; Score 33; DB 9; Length 67;

Best Local Similarity 85.7%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
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Db 46 GHPLDK 52

RESULT 14

Q9RXW3 PRELIMINARY; PRT; 225 AA.
AC Q9RXW3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE MUTT/NUDIX family protein.
GN DR0192.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Panphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans RI";
RL Science 286:1571-1577(1999).
DR EMBL: AE001881; AAF09779.1; -
DR TIGR: DR0192; -
DR InterPro: IPR000086; NUDIX_hydrolase.
DR Pfam: PF00293; NUDIX; 1.
DR PRINTS: PR00502; NUDIXFAMILY.
KW Complete proteome.
SQ SEQUENCE 225 AA; 24658 MW; BDD7BFE629AB7EBB CRC64;

Query Match 80.5%; Score 33; DB 16; Length 225;

Best Local Similarity 85.7%; Pred. No. 60;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
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Db 178 GHRELDK 184

RESULT 15

Q983T8 PRELIMINARY; PRT; 226 AA.
AC Q983T8;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Probable glutathione S-transferase.
GN MLR8180.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yanada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003013; BAB53792.1; -.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF02798; GST_N; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 226 AA; 25616 MW; 739F465BBBD0F670 CRC64;

Query Match 80.5%; Score 33; DB 16; Length 226;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHRPLD 6
Db 132 GHRPLD 137

Search completed: June 16, 2003, 16:04:30
Job time : 25.4 secs

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OM protein - protein search, using sw model

Run on: June 16, 2003, 16:04:34 ; Search time 27.5333 Seconds
(without alignments)
27.182 Million cell updates/sec

Title: US-09-424-940A-1

Perfect score: 41

Sequence: 1 GHRPLDK 7

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Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues
Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap:
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap:
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pap:
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap:
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	20	9	US-10-142-935-6
2	41	100.0	25	9	US-10-142-935-4
3	41	100.0	30	9	US-10-131-543-5
4	41	100.0	30	9	US-10-131-346-5
5	41	100.0	30	9	US-10-131-546-5
6	41	100.0	491	9	US-10-017-724-6
7	36	87.8	10	9	US-10-142-935-9
8	36	87.8	15	9	US-10-142-935-8
9	36	87.8	20	9	US-10-142-935-5
10	35	85.4	1203	10	US-09-799-875-5
11	32	78.0	855	9	US-10-072-094-9
12	32	78.0	855	10	US-09-817-913-13
13	32	78.0	855	10	US-09-817-538-13
14	32	78.0	967	9	US-09-563-728A-30
15	32	78.0	967	10	US-09-817-913-7
16	32	78.0	967	10	US-09-817-538-7
17	32	78.0	1084	9	US-10-072-094-7
18	32	78.0	1084	9	US-10-173-539-12
19	31	75.6	66	10	US-09-071-838-296

20	75.6	228	10	US-09-815-242-12032	Sequence 12032, A
21	75.6	384	10	US-09-825-414-54	Sequence 54, Appl
22	75.6	385	9	US-10-147-003-2	Sequence 2, Appl
23	73.2	68	9	US-10-102-806-465	Sequence 465, App
24	73.2	117	9	US-09-975-719-33	Sequence 33, Appl
25	73.2	294	9	US-09-738-626-4538	Sequence 4538, Ap
26	73.2	313	9	US-09-764-891-4243	Sequence 4243, Ap
27	73.2	359	9	US-10-060-036-179	Sequence 179, Appl
28	73.2	359	12	US-10-029-654-12	Sequence 12, Appl
29	73.2	363	10	US-09-815-242-11949	Sequence 11949, A
30	73.2	412	10	US-09-815-242-11978	Sequence 11978, A
31	73.2	463	10	US-09-858-075A-2	Sequence 2, Appl
32	73.2	597	10	US-09-828-313-38	Sequence 38, Appl
33	73.2	1507	9	US-10-043-487-330	Sequence 330, App
34	70.7	54	10	US-09-864-761-34308	Sequence 34308, A
35	70.7	57	10	US-09-864-761-34535	Sequence 34535, A
36	70.7	256	10	US-09-350-874-32	Sequence 32, Appl
37	70.7	297	9	US-09-738-626-5528	Sequence 5528, Ap
38	70.7	297	9	US-09-738-626-5574	Sequence 5574, Ap
39	70.7	460	9	US-09-464-099A-50	Sequence 50, Appl
40	70.7	460	10	US-09-861-696-50	Sequence 50, Appl
41	70.7	715	9	US-10-028-072-116	Sequence 116, App
42	70.7	715	9	US-10-121-049-116	Sequence 116, App
43	70.7	715	9	US-10-123-904-116	Sequence 116, App
44	70.7	715	9	US-10-140-470-116	Sequence 116, App
45	70.7	715	9	US-10-175-746-116	Sequence 116, App

ALIGNMENTS

RESULT 1
US-10-142-935-6
; Sequence 6, Application US/10142935
; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED C
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-6

Query Match 100.0%; Score 41; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 10 GHRPLDK 16

RESULT 2
US-10-142-935-4
; Sequence 4, Application US/10142935
; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072

; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-4

Query Match 100.0%; Score 41; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 15 GHRPLDK 21

RESULT 3

US-10-131-543-5
; Sequence 5, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT APPLICATION NUMBER: US/10/131,543
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-543-5

Query Match 100.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 4 GHRPLDK 10

RESULT 4

US-10-131-346-5
; Sequence 5, Application US/10131346
; Publication No. US20030103899A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-346-5

Query Match 100.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 4 GHRPLDK 10

RESULT 5

US-10-131-546-5
; Sequence 5, Application US/10131546
; Publication No. US20030103895A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
; FILE REFERENCE: 09744-018001
; CURRENT APPLICATION NUMBER: US/10/131,546
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
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; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: AMIDATION
; LOCATION: 30
US-10-131-546-5

Query Match 100.0%; Score 41; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
Db 4 GHRPLDK 10

RESULT 6

US-10-017-724-6
; Sequence 6, Application US/10017724
; Publication No. US20030099958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-017-724-6

Query Match 100.0%; Score 41; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
DB 45 GHRPLDK 51

RESULT 7

US-10-142-935-9
; Sequence 9, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:

; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-10-142-935-9

Query Match 87.8%; Score 36; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
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DB 5 GHRPLD 10

RESULT 8

US-10-142-935-8
; Sequence 8, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:

; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-10-142-935-8

Query Match 87.8%; Score 36; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6

DB | | | | |
10 GHRPLD 15

RESULT 9

US-10-142-935-5
; Sequence 5, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:

; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.

; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
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; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-10-142-935-5

Query Match 87.8%; Score 36; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
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DB 15 GHRPLD 20

RESULT 10

US-09-799-875-5
; Sequence 5, Application US/09799875
; Patent No. US20020034780A1
; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. US20020034780A1 Human Protein Kinases and Uses
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-799-875-5

Query Match 85.4%; Score 35; DB 10; Length 1203;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
| | | | |
DB 799 GHRPLSK 805

RESULT 11

US-10-072-094-9
; Sequence 9, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:

; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-094-9

Query Match 78.0%; Score 32; DB 9; Length 855;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 437 GHRPLSR 443

RESULT 12

US-09-817-913-13
; Sequence 13, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-817-913-13

Query Match 78.0%; Score 32; DB 10; Length 855;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 437 GHRPLSR 443

RESULT 13

US-09-817-538-13
; Sequence 13, Application US/09817538
; Patent No. US20020137162A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Antisense oligonucleotide Inhibition of Specific Histone
; FILE REFERENCE: 106101.144
; CURRENT APPLICATION NUMBER: US/09/817,538
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-817-538-13

Query Match 78.0%; Score 32; DB 10; Length 855;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 437 GHRPLSR 443

RESULT 14

US-09-563-728A-30
; Sequence 30, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zuomei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-728A-30

Query Match 78.0%; Score 32; DB 9; Length 967;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 506 GHRPLSR 512

RESULT 15

US-09-817-913-7
; Sequence 7, Application US/09817913
; Patent No. US20020061860A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zuomei
; APPLICANT: Bonfils, Claire
; APPLICANT: Besterman, Jeffrey
; TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
; FILE REFERENCE: 106101.145
; CURRENT APPLICATION NUMBER: US/09/817,913
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/192,157
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 967
; TYPE: PRT
; ORGANISM: Human
US-09-817-913-7

Query Match 78.0%; Score 32; DB 10; Length 967;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db ||||| :
506 GHRPLSR 512

Search completed: June 16, 2003, 16:16:36
Job time : 28.5333 secs